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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

AUTHORS TITLE	REFERENCE	JOURNAL	TITLE	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	AB001381	
Yokoyama, E. Direct Submission	97438227 2 (bases 1 to 480)	Biochim. Biophys. Acta 1353 (2), 103-106 (1997)	Cloning and sequencing of the hup gene encoding the histone-like protein HSl of Streptomyces lividans	Yokoyama, E., Doi, K. and Ogata, S.	1 (sites)	Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.	Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;	Streptomyces lividans	Streptomyces lividans (strain:TK24) DNA.	HSl protein; hup; histone-like protein.	AB001381.1 GI:2104559	AB001381	s DNA for HSl protein, complet	AB001381 480 bp DNA BCT 16-JUN-1999		

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                                                                                                                              Caulobacter crescentus.
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Cloning and sequencing of the hup gene encoding
protein HSl of Streptomyces lividans
Biochim. Biophys. Acta 1353 (2), 103-106 (1997)
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Submitted (10-OCT-1999) to the DDBJ/EMBL/GenBank databases. Yokoyama, Kyushu University, Faculty of Agriculture, Institu Genetic Resources, Microbial Genetics Division; Hakozaki 6-1 Higashi-ku, Fukuoka, Fukuoka 812-8581, Japan
                                                                                                  3 (bases 1 to 2327)
Yokoyama, E., Doi, K. and Ogata, S
Direct Submission
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Disruption of the hup gene encoding the
Streptomyces lividans
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                        652 CATCCCCGGCTTCCTGACTTTCGAGCGCACCCACCGTGCCGCCTCGCACCGCCACCCCAACCC
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                                                                                                                                                                                                                       CAAGCTCAAGGAAGCCGCCA 791
                                                                                                                                                                                                                                                                                                                         gcgcactggcgagcagattgacattccggcttcctacggcgttcgtatctccgctggctc 446
                                                                                                                                                                                                                                                                                               GCAGACCGGCGAGCCGATCCAGATTCCGGCCGGCTACAGCGTCAAGGTCTCCGCGGGCTC
AL138851.1 GI:6911971 bl-functional transferase/deacetylase; carboxy-terminal processing protease precursor; cell division ATP-binding protein; cell division protein; chain release factor 2; DNA binding protein;
                                                                                   Streptomyces
AL138851
                                                                                                                         SCE59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         348
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TVYESRLGFTSALNOWGAHIOLYRECLGGSDCRFGQRNFLHSAVVSGFTKLEGADLVI
PDLRGGFSYLIAALAAQGTSRVHGILINRGYENFMDKLVELGAKVELFGKALG"
787 c 836 g 356 t
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complement(987. .2327)
/gene="murA"
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ILFGGPLLHRLGHAF IPGLGGCD IGGRP IDFHFDVLRQFGAK IEKRADGQYLEAPQRL
RGTK INLPYPSVGATEGVLLTAVLAEGVTELSNAAVEPEIEDLICVLQKNGAI IANDT
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/protein_id="BAA85335.1"
/db_xref="GI:6063409"
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/transl_table=11
/product="histone-like protein HS1"
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/db_xref="GI:6063408"
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/strain="TK24"
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                                                                                                                       35856 bp
                                                                                                         coelicolor
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Pred. No.
                                                                                                                         DNA
                                                                                                         cosmid E59.
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REFERENCE
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JOURNAL MEDLINE REFERENCE AUTHORS
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TITLE
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   SGS
                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.

The length in codons is given for each CDS.

Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon.

Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at http://www.nih.go.jp/
jun/cgj-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.

1 (bases 1 to 35856)
Redenbach,M., Kieser,H.M., Denapaite,D., Eichner,A., Cullum,J., Kinashi,H. and Hopwood,D.A.
Kinashi,H. and Hopwood,D.A.
A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome Mol. Microbiol. 21 (1), 77-96 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     overlapping sections once,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequenced clone.
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by the BBSRC and Beownif Genomics
Details of S. coelicolor sequencing at the Sanger Centre are
available on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 7UH, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 (bases 1 to 35856) Cerdeno, A.M., Parkhill, J., Barrell, B.G. and Rajandream, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UDP-N-acetylglucosamine transferase. Streptomyces coelicolor A3(2). Streptomyces coelicolor A3(2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (URL; http://www.sanger.ac.uk/Projects/S_coelicolor/)
CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary)
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                                                                                                                                                                                                                                                                                                                                                                                                                               overlap between neighbouring submissions.
                                                                                                                                                                                                                                                                                                                                                                                                        E59
                                                                                              /db_xref="taxon:100226"
/clone="cosmid E59"
complement(1. .352)
/gene="SCE59.01c"
complement(1. .352)
                                                                                                                                                                                                                                                     /organism="Streptomyces
/strain="A3(2)"
                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                          'note="nominal overlap with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or longer,
                                                                                                                                                                                                                                                                                   coelicolor A3(2)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 because we arrange for
                                 coelicolor
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/note="SCE59.03c, possible sugar transporter inner membrane protein, len: 281 aa; sinilar to TR:CAB59590 (EMBL:AL132662) Streptomyces coelicolor putative sugar transporter inner membrane protein SCF11.13, 285 aa; fasta scores: opt: 730 z-score: 883.7 E(): 0; 42.1% identity in 278 aa overlap and to TR:AART1008 (EMBL:AE001988) Deinococcus radiodurans ABC transporter, permease protein, MalFG family DR1436, 283 aa; fasta scores: opt: 645 z-score: 781.7 E(): 0; 38.2% identity in 772 aa overlap. Contains Ffam match to entry pF00528 BPD transp, Binding-protein-dependent transport systems inner membrane component and match to Prosite entry PS00402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="SCE59.02c, probable sugar hydrolase, len: 545 aa; similar to TR:092H39 (EBML.AF072374) Pseudoalteromonas sp. S9 beta-N-acetylglucosaminidase (ChiQ, 788 aa; fasta scores: opt: 1378 z-score: 1537.3 E(): 0; 41.6% identity in 512 aa overlap and to SW:HEX1_VIBFU (EMBL:U41417) Vibrio furnissii beta-hexosaminidase (EC 3.2.1.52) EXOI, 611 aa; fasta scores: opt: 1023 z-score: 1142.5 E(): 0; 40.0% identity in 487 aa overlap. Contains Pfam match to entry PF0072B Glyco_hydro_20, Glycosyl hydrolase family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (EMBL:AL034492) Streptomyces coelicolor putative oxidoreductase subunit SC6C5.06, 296 aa; fasta scores: opt: 23 z-score 268.2 E(): 1.6e-07; 37.6% identity in 93 aa overlap and to TR:P95637 (EMBL:U65440) Rhodopseudomonas palustris 4-hydroxybenzoyl-CoA reductase Hbab subunit, 327 aa; fasta scores: opt: 193 z-score: 233.2 E(): 1.4e-05; 42.6% identity in 94 aa overlap*
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AAARAGHDVVMCPEQQVYLNFREDGGEDEPVPIAFVRTLEDVYRFEPVPAELTPEESG
HVIGTQANLWTEVTENQERVDYQLFPRLAAFAEYAWSALPAPADRDYAAFERRMATHY
RRLDALGVAYRPPAGFRPWQRRPGVLGRPMDGFPPNK"
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ERWLRATLGAATGLPLAPGEGGGGAVRLSLDGELADEGYRLDIAPDGVRLTGGGPAGL
FWGAQTLRQLLGPDAFRRAPLPGRRWRLPLGRIEDAPRFGWRGLMLDVSRHFMPKDGV
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/db_xref="GI:6911973"
/translation="""
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                                                                        Binding-protein-dependent comp sign. Contains possik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycosyl hydrolase
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/gene="SCE59.02c"
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PHGGYYTQEDIREIVAYAAARHITVLPEIDVPGHSQAAIAAYPELGNTDVIDTTALSV
WDTWGVSPNVLAPTENTLRFYEGVFEEVLELFPSEFVHIGGDECPKDQWRASATAQAR
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/note="screen
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complement/[/
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GGTDLMAAVNSGQLRPAALVGLGRISEIRGWQYQDGHALLGAGLTHARMGRPDFAALI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="SCE59.03c"
/note="screen
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complement/^^^
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/protein_id="CAB72188.1"
/db_xref="GI:6911972"
'codon_start-1
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Glycosyl hydrolase family 20, score 199.70, E-value
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/gene="SCE59.01c"
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/gene="SCE59.04c"
/note="SCE59.04c"
/note
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Binding-protein-dependent transport systems inner membrane
component, score 58.90, E-value 1.1e-13"
complement(2474. .2560)
/gene-"SCE59.03c"
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/db_xref="G1:6911975"
/db_xref="G1:6911975"
/taanslation="MSSGGVVRGRVRRRRGLSRSSPRPFRGSSSTPWLYLAPALVVLG
/translation="MSSGGVVRGRVRRRRGLSRSSPRPFRGSSSTPWLYLATVVFAA
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/gene="SCE59.04c"
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IESSEPRWYTIPSLDSFRRYVEQQEEGYYFLNSLIVAGSVVLASALIAFLAATAVTR
FRRFRTTLLIMETUAQMVPVEALT IPLFFIMEDFGQLUTLGSLILPHIAFSLPFAI
MLRGFVKAVPEALEEAAYIDGASRTRFLWQILFPLVLPGLVATSVFSFISTWNDFLFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SQWRIWRSVLAPMLRPILVVVTIQSVIWDFKVFTQIYVMTNGGGIAGQNMVLNVYAYQ
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/note="""
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/db_xref="GI:6911974"
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Pred. No. 1.2e-09;
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Nierman, W.C., Feldblyum, T.V., Paulsen, T.T., Nelson, K.E., Eisen, J., Neldelberg, J.F., Alley, M.R.K., Ohta, N., Maddock, J.R., Potocka, I., Heidelberg, J.F., Alley, M.R.K., Ohta, N., Maddock, J.R., Potocka, I., Nelson, W.C., Newton, A., Stephens, C., Phadke, N.D., Ely, B., Laub, M.T., DeBoy, R.T., Dodson, R.J., Durkin, A.S., Gwinn, M.L., Haft, D.H., Kolonay, J.F., Smit, J., Craven, M., Khouri, H., Shetty, J., Berry, K., Utterback, T., Tran, K., Wolf, A., Vamathevan, J., Ermolaeva, M., White, O., Salzberg, S.L., Shapiro, L., Venter, J.C. and
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Nierman, W.C., Feldblyum, T.V., Laub, M.T., Paulsen, I.T., Nelson, K.E., Elsen, J., Heidelberg, J.F., Alley, M.R.K., Ohta, N., Maddock, J.R., Elsen, J., Heidelberg, J.F., Alley, M.R.K., Ohta, N., Phadke, N.D., Potocka, I., Nelson, W.C., Newton, A., Stephens, C., Phadke, N.D., Ely, B., DeBoy, R.T., Dodson, R.J., Durkin, A.S., Gwinn, M.L., Haft, D.H., Kolonay, J.F., Smit, J., Craven, M., Khouri, H., Shetty, J., Berry, K., Utterback, T., Tran, K., Wolf, A., Vamathevan, J., Ermolaeva, M., White, O., Salzberg, S.L., Venter, J.C., Shapiro, L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (31-JAN-2001) The Institute for Genomic Medical Center Dr. Rockville, MD 20850, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete genome sequence of Caulobacter crescentus Proc. Natl. Acad. Sci. U.S.A. 98 (7), 4136-4141 (2001)
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AE005869 AE005673
AE005869.1 GI:13423417
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                                                                                                                                                                                                                    /translation="mrhladmtsaalppisvldlapvpogssygoalrnsidlaohae
TLGFHRYWLAEHHNWPGIASAATAVVIGOIAAATTTIRVGSGGVMLPNHAPLMVAEOF
GTLNALYPGRIDLGLGRAPGTDOATMTALRRYAGAVDSFAQDVVELQHWFKPASTDOS
                       complement(1417. .2625)
/gene="CC1958"
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/gene="CC1958"
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407...
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272. .348
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272. .
                                                                                                                                                                                                                                                                                               /product="conserved hypothetical protein"
/protein_id="AAK23932.1"
/db_xref="GI:13423418"
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407. .1420
                                                                                                                                                   GELAGLDHTLQYAAIGSPETVRRKIDRVLELTGADELMAAAQIHDHAARRRSYEILAS
                                                                                                                                                                           ESLDRPYAMVCIGVCAADTDEEAKRLSTSTQQQFLALRRGRPGLLPPPVDDIREHASP
note-"identified
                                                                                                                                                                                                    VRAVPGEGQDVPIWILGSSTWGAQLAAALGLPYAFAAHFAPDALIEALTLYRRHFKPS
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                                                                                                  .2625)
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  by match
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protein family HMM"
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ASVPPQGGRKHPQQEFLQVDTTNILFICGGAFAGLEKIISARGAAKSIGFGAKVTDPE
ERRTGEILKNVEPDDLQRFGLIPEFIGRLPVVATLEDLDEAALVKILTEPKNAFVKQY
                                                                                                                                                                                                                                                              /product="ATP-dependent Clp Clpx"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(6325. .7587)
/gene="CC1961"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYLEVDYDLSQVMFVTTANSLNMPQPLLDRMEIIRIPGYTEDEKLEIAKRHILPKLAK
DHGLKPAEFIVPDKAIRDLIRYYTREAGVRSLERELGALARKTVRDLAREKVASITID
DERLAKYAGVKKYRYGETDEVDQVGIVTGLAMTEFGGDILTIEAVKMPGKGRMQITGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KTQREVYLMEQMKATQREIGDPDDARDELIDLEKRIKKTKLSKEARTKAESELKKLRN
MSPMSAESTVVRNYLDWLLSIPWGKAKTKKIDLVESEGILDKYLEKVKERILEYL
AVQARTNSLKGPILCLVGPPGVGKTSLGKSIAKATGREFVRMSLGGVRDEAEIRGHER
TYIGSMPGKVVQSMKKAKTTNAFVLLDEIDKMGSDYRGDPASALLEVLDPSQNSTFGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QILLVTQKNSADDDPAPGDIFEVGVLATVLQLLKLPDGTVKVLVEGKARAAVVSFTDQ
ESYYEAQIGEVSEDDGAGPEAEALSRAVVEQFENYVKLNKKVPPEALASIPQIAEPGK
LADSIAAHLSVKIGDKQNLLEIFDVVKRLEKVFALMEGEISVLQVEKKIRSRVKRQME
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LVGFGTFKAVTRAAGTARNPRTGETVNRPASKTARFQVGEGLKSSLNS"
complement(3531. .5930)
                                                                                                                                                                                                                                                                                                                                                                                                      TIGR00382"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(6325.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LKDVMKESTAAANSYVRSRALQFGIKPPVFEKTDVHIHVPDGATPKDGPSAGIAMALA
MVSVLTGIPIRKDIAMTGEITLRGRVTAIGGLKEKLLAALRSGVKTVLIPQENEKDLA
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/gene="tRNA-Val-1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="CC1961"
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/transl_table=11
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TARTCCCCGTACCGGTGAGACCGTCAACCGTCCCGCGTCCAAGACGGCCCGCTTCCAGGT 3143
                                                                                          cgaggctgctgttaacgccttccaggatgtgttcgtcgaggctatgaagtccggcgaagg 320
                                 caacccgcgcactggcgagcagattgacattccggcttcctacggcgttcgtatctccgc 440
                                                                                                                                            CAAGGACGCGCTGGAAGCCTTTATCGAAGCGGTTACGGACTCGCTGAAATCGGGCCAAGA 3263
                                                                         152;
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QAQQVFDMYRQRADLQAALRAP I YEDKVVDL I FGKAK I EEKEVSKDELLEEDDL PEGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GKSLKAKDGDQLLIDFYGTIDGYEFAGGKAEGAELYLGSGQFIPGFEDQLYGAKPGDD
VYVKYKFPEEYQAKDLAGKDAEFATKYQEYRAPYDGKADDELAKRLGLSDLAALTELL
KSNLAGRYDNSSRFKLKRALLDYLDTKHDFPLPPRMYDAEFAGIWQQYEADKARGGLP
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AGGEDLSFDLAVEVMPEFEPIDPTSIELVKPYYKVSDEEVQEALDELAKQARTYEPRT
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/gene="CC1964"
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GMAASMGSLLLAAGAAGQRISLPNARIMVHQPSGGFRGQASDIERHAEDIIKTKRRLN
EIYVKHCGRTYEEVERTLDRDHFMSADEAKAWGLVDHVYDSRDAAEAGAE"
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RGWRAKGAKWYIVTASPDLIVAPFARGIGADLLIGTRLECSDGGRILGGIDGNNCRAK
EKVIKLREVEGPDVRLTAAYGDTSGDTEMLAIADEKGYRIFRGKPA"
complement(8670. 9302)
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/db_xref="GI:13423424"
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7971. .8591
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Pred. No. 3.2e-09;
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Burkholderia pseudomallei
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Burkholderia pseudomallei strain 1026b DbhB (dbhB), general secretory pathway protein D (gspD), general secretory pathway protein E (gspE), general secretory pathway protein E (gspE), general secretory pathway protein G (gspG), general secretory pathway protein G (gspG), general secretory pathway protein H (gspH), general secretory pathway protein I (gspJ), general secretory pathway protein J (gspJ), general secretory pathway protein K (gspK), general secretory pathway protein M (gspM), and general secretory pathway protein M (gspM), and general secretory pathway protein M (gspM), and general secretory pathway protein M (gspM), general secretory pathway protein M (gspM), and general secretory pathway protein M (gspM) general general secretory pathway protein M (gspM) general secretory pathway protein M (gspM) general secretory pathway protein M (gspM) general general secretory pathway protein M (gspM) general gener
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DeShazer, D., Brett, P. J.; Burtnick, M.N. and Woods, D.E.
Molecular characterization of genetic loci required f
of exoproducts in Burkholderia pseudomallei
J. Bacteriol. 181 (15), 4661-4664 (1999)
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                                                                                                                                                                                                                                                                                    'note="GspF"
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HSPSRCRYAETFTFVDDDGSTIADVARLDTMVTVIDAFNFLHDYARDDALAEHGLAAT
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Best Local :
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262 gaggctgctgttaacgccttccaggatgtgttcgtcgaggctatgaagtccggcgaaggc 321
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                                                                                                       202 aacaagtctgacctcgtttcgaagatcgcccagaagtccaacctgaccaaggctcaggcc 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="general secretory pathway protein
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TLGILTAAGVPILRALQAAGETLSNRAMRGNIDDAIVRVREGSALSRALNNVKTFPPV
LVHLIRSGEATGDVTTMLDRAAECESRELERRTMFLTSLLEPLLILAMGGIVLVIVLA
                                                                                                                                                                                                                                                                                                                                                                                                                     'db_xref="GI:4139242"
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/gene="gspC"
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NALKQKILLAFTYPA IVTVIAFGIVTFLLSYVVPQVVNVFASTKQQLFYLTIVMMALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note="GspG"
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                                                                                                                                                          0;
                                                                                                                                                                          Score 75.2; DB 1;
Pred. No. 1.5e-07;
                                                                                                                                                          Mismatches
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                                                                                                                                                                                                Length 20302;
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                                                                                                                                                 Gaps
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gene (KLDFEMIEIG" GKLDFEMIEIG" GRAFINATION GENERGHPEEGIEAGIRMEDVPEDMLCCPDCGV GRAFINATION COMplement(44174818) /gene="pA5352" /gene="pA5352" /codon_start=1 /transl_table=11 /product="conserved hypothetical protein" /product="conserved hypothetical protein" /protein_id="AAG08737.1" /protein_id="AAG08737.1" /ftanslation="MHSKFVLGAAREEAQRQGWAVSIAVVDDGGHPLAL /translation="MHSKFVLGRAEEDARVGRAFELSVPLLQATLEGGVPI /translation="MHSKFVLGRAEEDARVGRAFELSVPLLQATLEGGVPI /translation="MHSKFVLGRAEEDARVGRAFELSVPLLQATLEGGVPI /translation="MHSKFVLGRAEEDARVGRAFELSVPLLQATLEGGVPI /translation="MHSKFVLGRAEEDARVGRAFELSVPLLQATLEGGVPI /translation="MHSKFVLGRAEEDARVGRAFELSVPLLQATLEGGVPI /translation="MHSKFVLGRAEEDARVGRAFELSVPLLQATLEGGVPI /translation="MHSKFVLGRAEEDARVGRAFELSVPLLQATLEGGVPI /translation="MHSKFVLGRAEEDARVGRAEEDARVGRAFELSVPLLQATLEGGVPI /translation="MHSKFVLGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEGURVGRAEGURVGRAEEDARVGRAEEDARVGRAEEDARVGRAEEDARVGRAEGURVGRAEGURVGRAEGURVGRAEGURVGRAEGURVGRAEGURVGRAEGURVGRAEGURVGRAEGURVGRAEGURVGRAEGURVGRAEGURVGRAEGURVGRAEGURVGRAEGURVGRAEGURVGRAEGURVGRAEGURVGRAEGURVGRAEGURVGRAEGURVGRAEGURVGRAEGURVGRAEGURVGRAEGURVGRAUEG	complement(4164283) /gene="PA551" /codon_start=1 /transl_table=11 /protein_td="rubredoxin" /protein_td="%AG08736.1" /db_xref="GI:9951671"	/product="rubredc /protein_1d="Aage /db_xref="g1:995] /db_xref="g1:995] /translation="MRR /translation="MRR GKIDFENIEIA" GENDEMENTELAT Gene complement(4116. /gene-"PA5351"	CDS Gene	/Codon_start=1 /transl_table=11 /transl_table=11 /product="probable DNA-binding protein" /protein_id="AAGOB733.1" /protein_id="AAGOB733.1" /db_xref="GI:9951668" /db_xref="B11951668" /translation="MKKPELAAAIAEKADLTKEQANRVLNALLDEITGALNRKDSVTL VOFGTFLORHGARATGKNPOTGGPVKIKASNTVAFKPGKALRDAVN" gene vomplement(25593713) /gene="PA5349" CDS /gene="PA5349"	/gene="pA5347" /gene="pA5347" /gene="pA5347" /codon_start=1 /transl_table=11 /product="hypothetical protein" /protein_id="AAG08732.1" /protein_id="AAG08732.1" /db_xref="g1:9951667" /translation="MKFELLIWMLGRIMARASRDNPAFQKQLEGKDLVFQLHTLDGKV ARHYLVRDLRVSSKRGTHPQPAFSLGFKDAYGFAAMTSKNPQLAFMQGIQNKDIQIQ GNPALVJRPQGLYVLKPKKAPEKKAA" gene complement(2085. 2357) /gene="PA5348" CDS /gene="PA5348" CDS /gene="A5348" CDS

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Query Match
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EGEAARLAALRGTEADFVLLARRYEEMLASHEETOPIDPREHARRDHAFHRAISEASH
NPVLVHTLOSLNELLLLSTVFASVNNLYHRPPOKROIDROHARLYAALREROPDOAORA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DFIHAGYPVDAAAILLCELDGVEADVHEDCERVRELFEAAGATSVRQAQDEAERQRFW
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HPLILFDANLAGELERAEALGGRILELCVAVGGSITGEHGVGREKINQMCAQFNADEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             **Cranslation="MNILYDERLDGPLPQVDKDGLLAELRLRDDLEILHAAEDLRPY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RPVAGEPLALAEHRGIVAYDPCELVITARAGTPLDELQAVLARGGQMLACEAPGFGGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="glycolate oxidase subunit GlcE"
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AAARDLVEVLRDEPLESLGLRCDQRLAFHCPCTLQHAQRLGGAVEAVLRRLGFHLIEV
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   11.6%; Score 69.6;
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   DB
1;
Length 11691;
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δÃ

202 aacaagtetgaeetegtttegaagategeeeagaagteeaaeetgaeeaaggeteaggee 261

Query Match
Best Local Similarity
Matches 145; Conserv

Conservative

11.4%;

Score 68.2; DB 1; Pred. No. 9.3e-06; 0; Mismatches 128

Length 393; Indels

0;

Gaps

0

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JOURNAL
MEDLINE
REFERENCE
AUTHORS
TITLE
 BASE COUNT
ORIGIN
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SOURCE
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Hu,H.L. and Hong,G.F.
Direct Submission
Submitted (05-SEP-1998) Shanghai Institute of Biochemistry,Chinese
Submitted (05-SEP-1998) Shanghai Road, Shanghai 200031, China
                                                                                                                                                                                                                                                                                                                                                                                                                    J. Biol. Chem. 273 (32), 20568-20574 (1998) 98352101
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gene CDS	gene . CDS		gene	gene	gene CDS
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3068 ATCCGTCTCGCCGGCTTCGGCAGCTTCTCCGTAAGCCGTCGTGAAGCCCTCCAAGGGCCGT 3127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    202 aacaagtetgacetegtttegaagategeecagaagteeaacetgaceaaggeteaggee 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGCAAGGGCCTGAAGGACGCCGTCAACTCGTAAGGTT 3224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aacccgcgcactggcgagcagattgacattccggcttcctacggcgttcgtatctccgct 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCTTCCGCTGTTGATGCCGTATTCGAAACCGTACAGGGCGAACTGAAGAACGGTGGCGAC 3067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ggctccctgctgaagaaggccgtcaccgagtgacctt 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AACCCTTCCACGGGTGCTGAAGTCGATATCCCGGCTCGCAACGTGCCGAAGTTCTCCGCA 3187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ctgaagctcaccggcctgttctccgctgagcgcgtcaagcgcccggctcgcaccggccgc 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gaggctgctgttaacgccttccaggatgtgttcgtcgaggctatgaagtccggcgaaggc 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yokoyama, Kyushu University, Faculty of Agriculture, Institute o Genetic Resources, Microbial Genetics Division; Hakozaki 6-10-1, Higashi-ku, Fukuoka, Fukuoka 812-8581, Japan (E-mail:yokoyama@agr.kyushu-u.ac.jp, Tel:81-92-642-3059,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     histone-like protein.
Streptomyces lividans (strain:TK24) DNA.
Streptomyces lividans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AB032557 970 bp DN
Streptomyces lividans hup2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (20-SEP-1999) to the DDBJ/EMBL/GenBank databases. El-
submitted (20-SEP-1999) to the DDBJ/EMBL/GenBank databases. El-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Published Only in DataBase (1999) In press
2 (bases 1 to 970)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yokoyama, E., Doi, K. and Ogata, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Second histone-like gene hup2 of Streptomyces lividans TK24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yokoyama,E., Doi,K. and Ogata,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AB032557.1 GI:5926706
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/gene=
                                                                               /product="histone-like protein"
/protein_id="BAA84639.1"
/db_xref="GI:5926707"
                                                                                                                                                                                                                                                                                              /db_xref="taxon:1916"
272. ...928
                                                                                                                                                                                                                                                                                                                                                organism="Streptomyces/strain="TK24"
                                                                                                                                                             'transl_table=11
                                                                                                                                                                                        codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                ocation/Qualifiers
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                                                                                                                                                                                                                                                                hup2"
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Pred. No. 1e-05;
0; Mismatches 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene for histone-like protein,
                                                                                                                                                                                                                                                                                                                                                                            lividans"
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TITLE
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JOURNAL
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                   TITLE
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                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          316 gaaggcctgaagctcaccggcctgttctccgctgagcgcgtcaagcgcccggctcgcacc 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          326 CAGGCCGCCGACGCTGTCGACGCGGTCCTGGACGCCCTCGTCCGTGCGGTCGTCGCGGGC 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   256 caggccgaggctgctgttaacgccttccaggatgtgttcgtcgaggctatgaagtccggc 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     436 teegetggeteectgetgaagaaggeegteaceg 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      446 GCCCGCAACCCGCAGACGGGCGAGCGGGTTCGGGTCAAGAAGACCTCCGTGCCGCGCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  386 GACCGGGTCTCGGTCACCGGCTTCGGTTCCTTCGAGAAGGTCGACCGCCCGGCCCGGTTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122;
                                                                                                                                                                                                                                                                                                                                                                          Submitted (23-JUL-1998) Streptomyces coelicolor sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 7UH, UK
3 (bases 1 to 42210)
Redenbach, M., Kieser, H.M., Denapaite, D., Eichner, A., Cullum, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptomyces coelicolor A3(2).
Streptomyces coelicolor A3(2)
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3-isopropylmalate dehydratase large subunit; 3-isopropylmalate dehydratase small subunit; 3-isopropylmalate dehydrogenase; branched-chain amino acid aminotransferase; carboxyl transferase; delta-1-pyrroline-5-carboxylate dehydrogenase; gltX; glutamyl-tRNA synthetase; histone-like DNA binding protein; hydrolase; ilvE; sense; leuB; leuC; leuD; lyase; secreted lyase; transfer-RNA-Gln; leuB; leuC; lyase; secreted lyase; transfer-RNA-Gln;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                synthetase; histone-like DNA binding protein; nydroidse; ileuB; leuC; leuD; lyase; secreted lyase; transfer-RNA-Gln; transfer-RNA-Glu; ureAB; urease alpha subunit; urease beta and
                                                                                                                                                                                                                                                                                  A set of ordered cosmids and a detailed genetic and physical map
for the 8 Mb Streptomyces coelicolor A3(2) chromosome
Mol. Microbiol. 21 (1), 77-96 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Murphy, L. a. Unpublished
The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The lengt
                                                                    (URL; http://www.sanger.ac.uk/Projects/S_coelicolor/) CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                            97000351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Parkhill, J., Barrell, B.G. and Rajandream, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gamma subunits; ureC
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                                                                                                                                          Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.
                                                                                                                                                                                                                 Streptomyces coelicolor sequencing at The Sanger Centre is funded
                                                                                                                                                                                                                                                                                                                                                         Kinashi,H. and Hopwood,D.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Actinomycetales; Streptomycineae; Streptomycetaceae;
1 (bases 1 to 42210)
                                                                                                                                                                                           the BBSRC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                   misc_feature
                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                        misc_feature
```

dehydrogenases, score

/gene="SC1C2.01" /note="Pfam match

to entry PF00171 aldedh, Ald core 114.70, E-value 1.8e-30"

Aldehyde

/gene="SC1C2.01"

/note="PS00687 Aldehyde dehydrogenases glutamic acid

/note-"hairpin_loop with 18bp stem

/note="PS00070

Aldehyde dehydrogenases

cysteine active

'gene="SC1C2.01"

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Usually the highest scoring match found by fasta o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. General sequences are given to be a sequence of the codon o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prediction is based on positional base preference in codons using specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions. Cosmid IC2 lies between 8D9 and 7Al on the AseI-B genomic restriction fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             jun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of Bibb et al., Gene 30:157-66(1984) as implemented
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Acids Research,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="SCIC2.01"
/gene="SCIC2.01"
/note="SCIC2.01, probable delta-1-pyrroline-5-carboxylate
/note="SCIC2.01, probable delta-1-pyrroline-5-carboxylate
dehydrogenase, partial CDS, len >408 aa; similar to many
delta-1-pyrroline-5-carboxylate dehydrogenase (M.
tuberculosis) (543 aa), fasta scores; opt: 1753 z-score:
2214.2 E(): 0, 65.1% identity in 407 aa overlap, and
pur2_HUMAN delta-1-pyrroline-5-carboxylate dehydrogenase
(563 aa), fasta scores; opt: 1273 z-score: 1730.4 E(): 0,
48.5% identity in 408 aa overlap. Contains PS00687 and
PS00070 Aldehyde dehydrogenases glutamic acid acitive site
and cysteine active site and Pfam match to entry PF00171
aldedh, Aldehyde dehydrogenases, score 114.70, E-value
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="SC1C2.01"
<1. .1228
                                                                                                                                                                                                                                                                                              DFLVAHPSADRAVLKTALTRGAFEYQGQKCSATSRAYIPASIWNDGFKEEFAAEVDYL
TMGDVTDLSNFIGAVIDERSFAKNKAAIDRAKEDETCTIVAGGSYDDSVGYFVRPTVV
ECTDPENEVFRTEYFGPFLAVHVYDDSADDAYDAMLTQMESVSDYALTGSVISNDRAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="IDspcelidfwrenvhyarnilaeqppansqgvwnrmdhrpleg
fvyaitpfnfsaiaanlptapalmgnvvvwkpsptqthaavllmqlleeaglpkgvin
lvtgdgiavsevalehrdlagihftgstktfqhlwktvgnniekyrtypklvgetggk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="delta-1-pyrroline-5-carboxylate dehydrogenase"
/protein_id="CAA19968.1"
/db_xref="GI:3355668"
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/strain-"A3(2)"
/db_xref="taxon:100226"
                                                                                                                                                      KETLVAPTDYTYPHMG"
                                                                                                                                                                                                                          raytmeklryaagnfy indkstgavvgqqpfgggrasgtndkagapqnlmrwtltra i
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               /note="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="SPTREMBL:086502"
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true overlap with cosmid
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/translation="MTTPTIELKPSAHPLSDSERAAILANPGEGRHETDHMYTIKWTE
GRGWHEDGOLVPYAPLSLDPATWYLHYAQEIFEGLKAYKREPDGSVATFREEKNGARFQA
SSRRLGWPELPVDTFIEACDALVAQDEKWVPAHGGEESLYLRPFMIATEVALGYRPAN
EYLFIYIASPAGAYFPGGVKPVSIWVSEDRVRAVPGGWGDXGRGGNYAASLLAQARA
AKGCDQVCYLDAIERKWVEELGGMNLYFVYGNKIVTPSLTGSILEGVTRDSLLTVARD
                                                                                                                                                                                                                       /note-*SCIC2.04, ilvE, probable branched-chain amino acid aminotransferase, len: 362 aa; similar to many, e.g. ILVE_BACSU putative branched-chain amino acid aminotransferase (362 aa), fasta scores; opt: 1047 z-score: 1401.5 E(): 0, 44.7% identity in 360 aa overlap. Contains PS00770 Aminotransferases class-IV signature*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and isopropylmalate dehydrogenases signature and Pfam match to entry pr00180 isodh, isocitrate and isopropylmalate dehydrogenases.
                                                                                                                                /product="branched-chain
/protein_id="CAA19971.1"
/db_xref="GI:3355671"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LRPSKLLPGVATPLAGOPEIDFVVVREGTEGPYTGNGGTIRKGTEHEVATEVSVNTAY
GVERVVRDAFARAQARPRKKLTLVHKNNVLTFAGHLWTNIFNKVAAEYPEVTTDYLHV
DAATIFLVTDPARFDVIVTDNLFGDIITDLAAAVSGGIGVAASGNINPSGDFPSMFEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note-"SCIC2.03, leuB, probable 3-isopropylmalate dehydrogenase, len: 347 aa; similar to e.g. LEU3_CORGL 3-isopropylmalate dehydrogenase (EC 1.1.1.85) (340 aa), fasta scores; opt: 1450 z-score: 1318.1 E(): 0, 68.0% identity in 338 aa overlap. Contains PS00470 Isocitrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="PS00470 Isocitrate
dehydrogenases signature"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                isopropylmalate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MSRSLNLAVIPGDGIGQEVVAEGLKVLSAVLPQDVKLETKEFDF
GARRYHATGETLTDADLDALKAHDAILLGAIGDPSVPSGVLERGFLLKLRFAFDHHVN
                                                                                                          'db_xref="SPTREMBL:086505"
                                                                                                                                                                                           transl_table=11/
                                                                                                                                                                                                          codon_start=J
                                                                                                                                                                                                                                                                                                                                                                                                                                           'note="
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="Pfam match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="leuB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="3-isopropylmalate
/protein_id="CAA19970.1"
/db_xref="GI:3355670"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="hypothetical protein
/protein_id="CAA19969.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="SC1C2.02"
1537. .1668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HGSAPDIAGQGKADPTATVLSVALLLRHLGYEDEAARIEDAVSADLGERGDLPARST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    db_xref="GI:3355669"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               xref-"SPTREMBL:086504"
                                                                                                                                                                                                                                                                                                                                                                                                                   *possible RBS upstream of ilvE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . 2517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch to entry PF00180 isodh, Isocitrate and dehydrogenases, score 356.60, E-value
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dehydrogenases, score 356.60, E-value
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                                                                                                                                                                    amino acid aminotransferase"
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JOURNAL
MEDLINE
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                                                                                                                                                                                                                                                                                                                                                       AUTHORS
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                              21173698
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41235 CAGGCCGCCGACGCTGTCGACGCGGTCCTGGACGCCCTCGTCCGTGCGGTCGTCGCGGGC 41294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GACCGGGTCTCGGTCACCGGCTTCGGTTCCTTCGAGAAGGTCGACCGCCCGGCCCGTTAC 41354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gaaggcctgaagctcaaccggcctgttctccgctgagcgcgtcaagcgcccggctcgcacc 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCCCGCAACCCGCAGACGGGCGAGCGGGTTCGGGTCAAGAAGACCTCCGTGCCGCGCTTC 41414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caulobacter crescentus
AE005903 AE005673
                                                                                                                                                                                                                                                                                                   2 (bases 1 to 11684)
Nierman, W.C., Feldblyum, T.V., Paulsen, I.T., Nelson, K.E., Eisen, J., Nierman, W.C., Feldblyum, T.V., Ohta, N., Maddock, J.R., Potocka, I., Nelson, W.C., Newton, A., Stephens, C., Phadke, N.D., Ely, B., Nelson, W.C., Newton, A., Stephens, C., Phadke, N.D., Ely, B., Laub, M.T., DeBoy, R.T., Dodson, R.J., Durkin, A.S., Gwinn, M.L., Haft, D.H., Kolonay, J.F., Smit, J., Craven, M., Khouri, H., Shetty, J., Berry, K., Utterback, T., Tran, K., Wolf, A., Vamathevan, J., Berry, K., White, O., Salzberg, S.L., Shapiro, L., Venter, J.C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nierman, W.C., Feldblyum, T.V., Laub, M.T., Paulsen, I.T., Nelson, K.E. Eisen, J., Heidelberg, J.F., Alley, M.R. K., Ohta, N., Maddock, J.R., Potocka, I., Nelson, W.C., Newton, A., Stephens, C., Phadke, N.D., Ely, B., Deboy, R.T., Dodson, R.J., Durkin, A.S., Gwinn, M.L., Berty, B., Chonay, J.F., Smit, J., Craven, M., Khouri, H., Khothay, J.F., Smit, J., Wolf, A., Vamathevan, J., Berry, K., Utterback, T., Tran, K., Wolf, A., Vamathevan, J., Ermolaeva, M., White, O., Salzberg, S.L., Venter, J.C., Shapiro, L. and
                                                                                                                                                                                   Submitted (31-JAN-2001) The Institute for Genomic Research, Medical Center Dr. Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 11684)
Nierman, W.C., Feldbly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caulobacter crescentus
                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complete genome sequence of Caulobacter crescentus
Proc. Natl. Acad. Sci. U.S.A. 98 (7), 4136-4141 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AE005903.1 GI:13423852
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/gene="CC2328"
                                                         /organism="Caulobacter crescentus"
/db_xref="taxon:69394"
                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(4214.
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complement//^~.
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Pred. No. 1
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1.2e-05;
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229 of 359 of the complete
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/gene="CC2334"
6557. .7441
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SYSVEVLPPAVAKSSPPSKRVYVSIKQSGOLYLGDMETSIDELGYDITKNMGRRDP
SKERLFIRADEKVRYGAFMSVMNTLQDNGFYSVALVGRDDSQ"
complement(7805...8713)
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errlyrptyiymlgataafgvmgrptpvretrgrplplpdgvqglytfhpsyllrlpd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EPVTDAATTFVVPAAFMEMAQQVVLNRSLDRFÄLLYRILWRLEREPRLIENPADQDMA
RARDMAKAVSRAAHKMKAFVRFRRVEDAAKETYAAWFEPAHRVTEATAPFFARRFSNM
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RDDLKAVLSPAVQLSLF"
                                                                                              /product="MotA/TolQ/ExbB
/protein_id="AAK24307.1"
/db_xref="GI:13423861"
                                                                                                                                                                                                                                                                                complement(7805. .8713)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="hypothetical
/protein_id="AAK24305...
/db_xref="GI:13423859"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="trNA-His-1"
5557. .7441
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/protein_id="AAK24304.1"
QEVELSRQAGLAVAGEHRDSTLSRATYAINAVQSSLAKRLSGGMVFLASVGSGGPFIG
                           FSWVLLLTKIFEFAALNKQSDKFLEAFRGARSIADIARISSSEEFEGNPMADMAAAAS
                                                   DAAAAPAADAAAAAPAPEAAPAEEAAAPAAHSLTPIGMFMQAGVVVKVVMIGLVLASV
                                                                                                                                                                                                                                  /note="identified by match
                                                                                                                                                                                                                                                        /gene="CC2336"
                                                                                                                                                                                                                                                                                                           /gene="CC2336"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="similar to SP:Q05606 GB:X70139 PID:49194; Identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(7365. .7799)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="CC2335"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RQISEQQRVQTSHDGQGDTKGTETLLATWAFRRERIVAAMLGRILISHASPPTGYHPV
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/db_xref="GI:13423858"
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                                                                                                                                                                               transl_table=11
                                                                                                                                                                                                             /codon_start=:
                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="AAK24306...
/db_xref="GI:13423860"
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                                                                              translation="MLDIKRKTPFIALVGAMALMASAPAFAQDAAAPAAATAEAQPAT"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ctgagcgcgtcaagcgcccggctcgcaccggcgcaacccggcgcactggcgagcagattg 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCGCCGCCGACGAAAAACTGACGAAGACCCAGGCCAAGGCCATCATCGACGGCGTCTTCA 3299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tcgcccagaagtccaacctgaccaaggctcaggccgaggctgctgttaacgccttccagg 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ccgagtgacctt 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAATCGCCGCCAGCAAGAAGGTCGGCTTCACGCCGGCCAAGCAACTGAAGGACGCCGTCA 3479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGTCGATCTCCGACGCCGCCGTGAAGGGCGAGGAAGTCTCGATCCCCGGCTTCGGCAAGT 3359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 atgtgttcgtcgaggctatgaagtccggcgaaggcctgaagctcaccggcctgttctccg 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   al Similarity
136; Conserv
Submitted (16-MAY-2000) Department of Medicine and Genetics, University of Washington Genome Center, University Of Washington, Box 352145, Seattle, WA 98195, USA
                                                                                        Stover,C.K., Pham,X.*Q.T., Erwin,A.L., Mizoguchi,S.D., Warrener,P., Hickey,M.J., Brinkman,F.S.L., Hufnagle,W.O., Kowalik,D.J., Lagrou,M., Garber,R.L., Goltry,L., Tolentino,E., Westbrook-Wadman,S., Yuan,X., Brody,L.L., Coulter,S.N., Folger,K.R., Kas,A., Larbig,K., Lim,R.M., Smith,K.A., Spencer,D.H., Wong,G.K.-S., Wu,Z., Paulsen,I.T., Reizer,J., Saier,M.H., Hancock,R.E.W., Lory,S. and Olson,M.V.
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Garber,R.L., Goltry,L., Tolentino,E., Westbrock-Wadman,S., Yuan,Y.,
Brody,L.L., Coulter,S.N., Folger,K.R., Kas,A., Larbig,K., Lim,R.,
Smith,K., Spencer,D., Wong,G.K., Wu,Z. and Paulsen,I.T.
Complete genome sequence of Pseudomonas aeruginosa PA01, an
opportunistic pathogen
Nature 406 (6799), 959-964 (2000)
                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas aeruginosa
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AE004606 AE004091
AE004606.1 GI:99
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                                                                                                                                                                                                                                                                      (bases 1 to 10851)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             product="oxidoreductase,
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Pred. No. 1.
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Mismatches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       section 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         family"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLAIVHRVAQWHGGYAEALETPQGGASFRLTWERPR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note="PA1800"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'db_xref="GI:9947781"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .2077)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QEMGKKVGEAFKEVEPEDLVKFGLIPEFVGRLPVIATLDELDEAALMQILTEPKNALT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EIPDNIKSDLVIKPVKWIDEVLQIALQYAPEPLPD!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LGDVMAESITAALTVVRSRAQSLGIAADFHEKRDIHIHVPEGATPKDGPSAGIGMCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MSPMSAEATVVRSYIDWLLNVPWKAESKVRHDLAKAEDILDADHYGLEEVKERILEYL
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/transl_table=11
                                                                                                                                                                                                                                                                                                                                        transl_table=11/
                                                                                                                                                                                                                                                                                                                                                                                         'gene="ppiD"
                                                                                                                                                                                                                                                                                                                                                                                                                 note="PA1805"
907. .10772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'gene="ppiD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'product="tRNA-Asp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'gene="hupB"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="PA1803"
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8406 AACAAGTCGGAACTGATCGATGCAATTGCCGCATCTGCTGATATCCCGAAAGCTGTTGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ggctccctgctgaagaaggccgtcaccgagtgaccttct 480
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                                                                                                                                                                                                                          Submitted (14-JUN-2000) The Institute for Genomic Medical Center Dr. Rockville, MD 20850, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                          Sellers, P., McDonald, L., Utterback, T., Fleishmann, R. Nierman, W.C., White, O., Salzberg, S.L., Smith, H.O., CMekalanos, J.J., Venter, J.C. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Heidelberg,J.F., Eisen,J.A., Nelson,W.C., Clayton,R.A., Gwinn,M.L., Dodson,R.J., Haft,D.H., Hickey,E.K., Peterson,J.D., Umayam,L.A., Gill,S.R., Nelson,K.E., Read,T.D., Tettelin,H., Richardson,D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Heidelberg,J.F., Elseu,J.F., Peterson,J.D., Umayam,L., Dodson,R.J., Haft,D.H., Hickey,E.K., Peterson,J.D., Richardson,D., Gill,S.R., Nelson,K.E., Read,T.D., Tettelin,H., Richardson,D., Gill,S.R., Nelson,K.E., Read,T.D., Tettelin,H., Dragoi,I.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sellers, P., McDonald, L., Utterback, T., Fleishmann, R.D., Nierman, W.C. and White, O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Heidelberg, J.F., Eisen, J.A., Nelson, W.C., Clayton, R.A., Gwinn, M.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria;
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AE004115.1 GI:96
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                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                             Ermolaeva, M.D., Vamathevan, J., Bass, S., Qin, H., Dragoi, I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA sequence of both chromosomes of the cholera pathogen Vibrio
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/note="biotype: El Tor" complement(162. .1400)
                                                                                                                                          /organism="Vibrio cholerae"
/strain="N16961"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proteobacteria; gamma subdivision; Vibrionaceae;
                                                        /chromosome="I"
                                                                                     /db_xref="taxon:666"
                                                                                                                /serotype="01"
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Pred. No. 4.6e-05;
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m A} BCT 31-JUL-2000 I, section 23 of 251 of the complete
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/note="similar to SP:P25081 GB:X57117 PID:48820;
/note="similar to SP:P25081 GB:X57117 PID:48820;
                                                                                                                                                                                             /gene="VC0269"
3974. .5173
                                                                                                                                                                                                                                                                                              QITFMACLCERMYPNYAMFCEHTQFAEARIYRDILDSVWELMTVKNAKVNFEHQLEKL
EELIPTSDAFDLYAVYPAIDACEGLATLLHGLLDRDDLAESMIKVSQISVQTVAQLEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="VC0268"
2943. .3611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="mnnfholyIlteedehyreqilterqlegialtedrakatillaa
ppmaarrldefprlwihsatagvdtlmdpkleknylltnvkgifghllaeynmgai
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RTGIPakeghfdatyhIselpaalmradllvntlpntpategilnqenlrhchqallf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MLESLITEIRQCTVCEPHLPLGANPVIRAHPAAKILIIGQAPGT
KVHQTSIPWNDASERLRQWIGLDREAFYCEENIAIMEMGLCYGKGRGSGDLPPRKEC
APIMHAKVLEQLPHRQLTLLIGQYAQHYYLSDKPSTLTETVQQWQRWAPSVLPLPHPS
PRNTLWLKNHPWFEQDIVPYLRQRVKQVLT"
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YLRTHPNIHQDMTLMVRQLAPTHDGISLEVYCFTSTTVWVEYERIQSDIFDHIYAVLP
EFDLRVSQAPTGNDFRALRG"
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IGKSPVILLSGLGAMTAVFMLVFKDPILGLVAGVQLSANKMLSVGDWLEMPKYGADGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(2027. .2950)
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/gene="VC0266"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEQVVDIFADNYQRWCDNLPLRNQIDFEKGY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NVGRGKTLVEQGLPDLIAAGHIRHAFLDVFIKEPLAQDHPFWDNPAITITPHIAAVSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="D-isomer specific 2-hydroxyacid dehydrogenase
family protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(2027. .2950)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="conserved hypothetical protein"
/protein_id="AAF93441.1"
/db_xref="GI:9654676"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(1455. .2027)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VIDISLTTVKVQNWDKTITTIPSYALISDSFKNWKGMQESGGRRIKRSILIDATSVHF
                                                                                                                                                                                                                                                                                                                                                                                 translation="MFIGASFFPYGYPVHFRCLFPQRFEVTMLQNPLQLRLEKFEPWQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transl_table=11/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note-"identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="VC0268"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="AAF93442.1"
/db_xref="GI:9654677"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="similar to GB:Z11929 SP:P43169 PID:46871;
identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="VC0267"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="VC0266"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MLETLTLWLQKFDIEIERVIQLAEALGLIAAISIAIHLVLHRGV
LLWLKRHTHHEQSVWRNALFKEHLFSRVALLIQGVVIAVQTQLWLSPNTFAYDVLHTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="conserved hypothetical protein"
/protein_id="AAF93440.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="identified by Glimmer2; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transl_table=11
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/gene="VC0272"
7534. 7698
/gene="VC0272"
                                                                                                                                                                                                                                                               /note="similar to Sp:P28080 PID:141878; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                               /gene="VC0273"
7897. .8169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HRDTPFSRPLIYSEEKDNIVGFVHRLELFKEQQNGQGNLLLGDVMRPIHVVLNTLSLF
KAFDQMMQKRLQLSVVVDEYGSVQGLLTLEDIFEHLLGEEIIDEADRTTDMQQLATER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="conserved hypothetical protein"
/protein_id="AAF93446.1"
/db_xref="GI:9654681"
/tanslation="MFLLAIYISVAIGVSFICSVLEAVILSITPSYLAQLRQQGHPAA
NRLAGLKADIDRPLASILTLNTIAHTIGAATAGAQAAVVFGSOMLGLESAVITLGILV
LSEIVPKTIGATYWRELAPQASLVLRWMVWALTPFVWFSEQITKRLARKVEAPKLRDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MQQDVSREHTINNGSSMADHDEHPIEQKEFYMLIGLDIGGTKIE
ICVLDKQGSMLYRQRIATPDNYSQFVDCVCSLIVDAEQATQPVDSIGIGLPGAVSPVT
GLIKNANCTFLNGQDLSSDLQYRLGREVKLANDANCFALSEAIDGAGKESMYVFGAIL
                                                      /translation="mnktqLidfiAEKADLTKVQAKAALEATLGAVEGALKDGDQVQL
IGFGTFKVNHRSARTGRNPKTGEEIKIAAANVPAFVAGKALKDAIK"
                                                                                                                                                  /product="DNA-binding protein
/protein_id="AAF93448.1"
                                                                                                                                                                                                                                                                                                                               /gene="VC0273"
                                                                                                                                                                                                                                                                                                                                                                                                                                  7897...8169
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIEMTGFPVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="hypothetical protein"
/protein_id="AAF93447.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7534.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WEHWKRQHRMIESRDEVE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(6467. .7525)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTGCGGSIVVNRQVLVGPNAICGEWGHNPLPGYHLEQDGAARYCYCGRQNCIERFISG
SGFQDSYQALTGECITASEIMKRYKQQEPEAIHCYTQLIDHMARSFAGLVNVLDPDII
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PID:581151 GB:U00096; identified by sequence similarity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AKQPIFALIEELATQYPNDIGLFAPLMLHVLTLQPGEAMFLDARTPHAYLKGTALEIM
ANSDNVLRAGLTPKHIDVVELAKCTLFKEKSEATLLLTPIQQGDMLSFPVPVADFKFA
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wwgthpngcsyvefsgekiklstlieqkktdflsiqtveqfgelpylfkilaanqals
iqvhpskaeaeegfarenaqgilinatnrnykdpnhkpelvyaltnyqamngfrplsb
                                                                                                                      /db_xref="GI:9654683"
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'gene="VC0274"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        translation="MVLKCTFELFSSHNLRGKGRKAQGEYEEKSLRLKEPKVLFSVTK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'db_xref="GI:9654682"
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/protein_id="AAF93445.1"
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REFERENCE
AUTHORS
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VERSION
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AF167159
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                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                 REFERENCE
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                                                                                                                                                                                                            JOURNAL
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CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8020 GTACAACTGATTGGTTTTGGTACATTCAAAGTTAATCATCGTTCTGCTCGTACTGGCCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ctgaagctcaccggcctgttctccgctgagcgcgtcaagcgcccggctcgcaccggccgc 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AACAAGACCCAATTGATCGACTTTATCGCAGAGAAAGCGGACCTGACTAAAGTGCAAGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AATCCAAAGACCGGTGAAGAGATCAAAATTGCGGCAGCTAACGTTCCTGCATTCGTAGCA 8139
                                                                                                                                                                                                                                                                                                                                                                      Summers, M.L., Botero, L.M., Busse, S.C. and McDermott, T.R. The ++Sinorhizobium meliloti lon protease is involved in regulating exopolysaccharide synthesis and is required for nodulation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sinorhizobium meliloti
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (hupB) genes, complete AF167159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sinorhizobium meliloti Lon protease (lon) and histone-like (hupB) genes, complete cds.
                                                                                                                                                                               Submitted (08-JUL-1999) Land Resources and Environmental Sciences, Montana State University, 334 Leon Johnson Hall, Bozeman, MT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sinorhizobium meliloti.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AF167159.1 GI:6175840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AF167159
                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                      Summers, M.L.
                                                                                                                                                                                                                                                                                                       20225855
                                                                                                                                                                                                                                                                                                                          Bacteriol. 182 (9),
                                                                                                                                                                                                                                                                              (bases 1 to 3380)
                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 3380)
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NGTTGGKTIGDATSFYMYTESFQKPSSASDYVTSGDYGSYQTSYRMEEGQVREIRREG
EHLDGKKLVPFRVHIRFSKEGEAVYQQYRLGGKVLPMNEEQLAHYVLQAKAVAEATKE
QDKQGLELIQGYWNGKFFETCGGVEYQRVEFNQSLPSFVFNRLASIESYVAFLGKIRN
GKVHIDELLLLDDAGHDCVKEFELLD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(9004. .10293)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="hypothetical protein"
/protein_id="AAF93449.1"
/db_xref="GI:9654684"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="VC0275"
                                                               /organism="Sinorhizobium
/db_xref="taxon:382"
                                                                                                                                        ocation/Qualifiers
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                 no.
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                                                                                                                                                                                                                                                                                                                            2551-2558 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                by Glimmer2; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 12116;
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                                      ggctccctgctgaagaaggccgtcacc 468
                                                                                                  AACCCGTCGACGGGGGGGAAGTTGACATTCCGGCACGCGAACGTGCCGAAGTTCACGGCC 3234
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EIRGHRRTYIGSMPGKVVQSMKKAKKSNPLFLLDEIDKMGQDFRGDPSSALLEVLDPE
QNSTFMDHYLEVEYDLSNVMFTTTANTLNIPPPLMDRWEVFRIAGYTEEEKLEIAKRH
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IERYTPRDDFYEAMAHALPEPDEDPVEIEALSRSVVSEFESYVKLNKKISPEVVGVAS
QIEDYSKLADTVASHLSIKIVEKQEMLETTSVKMRLEKALGFMEGEISVLQVEKRIRS
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TKKVEVSAENINDYLGVPRFRHGEAERDDQVGVVTGLAWTEVGGELLTIEGVMMPGKG
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Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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AAN70753 AAC79661 AAA88001 AAQ70417 AAQ70418		AAF21609 AAF21610 1 AAA81490	ID
Sequence of segmen Virulence gene #68 Mycobacterium bovi Streptomyces chole Streptomyces chole	N. meningitidis pa Genomic fragment # Gum gene cluster.	Neisseria meningit Neisseria meningit Neisseria meningit	Description

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AAF15020	AAN91207	AAQ10499	AAA10594	AAF60958	AAT06312	AAQ73500	AAQ10543	AAQ10212	AAF30870	AAA13905	AAV23494	AAT93610	AAA13897	AAV23479	AAF30757	AAF13147	AAQ06095	AAX98060	AAX98061	AAH90842	AAA14651	AAT16480	AAX98035	AAX98058	AAX98059	AAZ11393	AAH90729	AAH90714	AAH49591	AAH48225	AAH44356	AAH27164	AAT49320
Trichoderma reesei	Beta-ketothiolase	ketothiolas	Gene encoding a su	P. putida KT2440-a	Thaumatin II synth	DNA encoding Pseud	BamHI J-I fragment	BamHI J-I fragment	Pseudomonas alcali	Pseudomonas alcali	Pseudomonas Xpc, O		Pseudomonas alcali	Pseudomonas XcpO s	Micromonospora meg	Aspergillus oryzae	Sequence encoding	Nucleotide sequenc	Nucleotide sequenc	2CFE 33 coding seg	Nucleotide sequenc	SA8 virus qB qlyco	Nucleotide sequenc	Nucleotide sequenc	Nucleotide sequenc	/accae ant	coding	CFE 14 coding sequ		Heart muscle cell	Human GATA4 nucleo	Streptomyces prequ	Cholesterol oxidas

ALIGNMENTS

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RESULT 1
AAF21609/c
ID AAF21609;
XX
AAF21609;
XX
AAF21609;
XX
AAF21609;
XX

DT 13-MAR-2001 (first entry)
XX

Neisseria meningitidis B nucleotide sequence SEQ ID NO:110.
XX

Neisseria meningitidis; Neisseria gonorrheae; immunogenic; vaccine; kW diagnosis; antigen; detection; infection; gene therapy; antibacterial; XX

KW

MC200066791-A1.
XX

OS

Neisseria meningitidis.
XX

Noisseria meningitidis.
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Noisseria meningitidis.
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OS

Neisseria meningitidis.
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Noisseria meningiti
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RESULT 2
AAF21610/c
ID AAF216
XX AAF216
AC AAF216
XX
DT 13-MAR
XX
DE Neisse
KW Neisse
KW diagno
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                                                                                       Neisseria meningitidis; Neisseria gonorrheae; immunogenic; vaccine; diagnosis; antigen; detection; infection; gene therapy; antibacteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bacteria. Computers, computer memory, computer storage medium or computer databases can be used in a search to identify open reading frames (ORFs) or coding sequences within the NMB genome. The DNA sequences provide further opportunities to find antigenic or immunogenic proteins which are more effective in vaccines than the outer membrane proteins currently
                                                                                                                                                                                                            13-MAR-2001
                                                                                                                                                                                                                                                          AAF21610;
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                     Neisseria meningitidis
                                                                                                                                                              Neisseria meningitidis B nucleotide sequence SEQ ID NO:111.
                                                                                                                                                                                                                                                                                                      AAF21610 standard;
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                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                      DNA;
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                                                                                          infection; gene therapy; antibacterial;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CC Neisseria meningitidis B (NMB). The sequences in AAF21544 and AAF21607 CC to AAF21613 represent fragments of the NMB genomic sequence, as the csequence was too long to go in a record on its own it was split into 8 CC sequences which overlap each other at the beginning and end of each CC sequence by 49980 bp (i.e. the last 49980 bp of AAF21544 is repeated at CC the beginning of AAF21608, and so on). AAF21545 to AAF21588 encode the CC Neisseria proteins given in AAB58550 to AAB58593, and AAF21589 to CC AAF21606 represent PCR primers which are used in the exemplification of CC AAF21606 represent invention. The NMB genome and fragments from it have CC entibacterial activity, and can be used in vaccines and gene therapy. CC Meisseria nucleic acids, proteins and/or antibodies which binds to the presence of Neisserial bacteria or as a diagnostic reagent for detecting the presence of Neisserial bacteria or of antibodies raised to Neisserial computer memory, computer Storage medium or computer CC databases can be used in a search to identify open reading frames (ORFs) or coding sequences within the NMB genome. The DNA sequences provide further opportunities to find antigenic or immunogenic proteins which are morely no effective in vaccines than the outer membrane morely no currently are
                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 127
                                                                                                                                                                                                                                                                                             35204 AACAAGTCTGAATTGATCGAAGCGATTGCTCAAGAAGCCGACATTTCCAAAGCCGCCGCA 35145
                                                                                                                                                                                                             35144 CAAAAAGCTTTGGATGCCACTACCAATGCAGTAACCACCGCCCTGAAACAAGGCGACACC 35085
                                                                                                                             35084 GTTACTTTGGTCGGTTTCGGTACTTTCTACGTGGGCGAACGTGCGGAACGCCAAGGCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          more effective in vaccines than the outer membrane proteins used.
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Galeotti C, Mora M,
Frazer CM, Grandi G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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08-OCT-1999;
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  442
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                                                                                                                                                                                                                                                      262
                                                                                                                                                                                                                                                                                                                 202 aacaagtctgacctcgtttcgaagatcgcccagaagtccaagctcgaccaaggctcaggcc 261
                                                                                                                                                                                                                                                                                                                                                                             y Match 7.9%;
Local Similarity 48.8%;
hes 127; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             present invention describes the full length genome of seria meningitidis B (NMB). The sequences in AAF21544
                                                                                                                                                           ctgaagctcaccggcctgttctccgctgagcgcgtcaagcgcccggctcgcaccggccgc 381
                                                                                                                                                                                                                                       gaggctgctgttaacgccttccaggatgtgttcgtcgaggctatgaagtccggcgaaggc 321
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ggctccctgctgaagaaggc 461
                                             AACCCCAAAACCGGCGAGCCTCTGACCATTGCCGCCGCCAAAACGCCTAAATTCCGCGCC 34965
                                                                                aacccgcgcactggcgagcagattgacattccggcttcctacggcgttcgtatctccgct 441
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99WO-US23573.
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                                                                                                                                                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                                                                                                                                                             Score 47.2; DB 21;
Pred. No. 0.0052;
0; Mismatches 133;
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, Scarselli M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genome sequence and open reading prevent Neisserial infections -
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Scarlato V,
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Rappuoli R;
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The present invention describes methods of obtaining immunogenic CC proteins from Neisseria genomic sequences. AAA81451 to AAA82414 CC represent specifically claimed Neisseria meningitidis genomic DNA CC sequences; AAA81260 to AAA81303 and AAB25620 to AAB2563 represent CC Neisseria DNA sequences and their corresponding proteins; AAA81254 to AAA81259 and AAA81304 to AAA8131 represent PCR primers used in the CC isolation of Neisseria meningitidis DNA sequences; and AAA81322 to AAA81452 represent Neisseria meningitidis MenB polynucleotide ORF CC Sequences, which are all used in the exemplification of the present CC invention. The nucleic acid sequences, protein sequences, and antibodies composition can be used in the manufacture of a composition. The composition can be used as a medicament (or in the manufacture of a CC Meisserial bacteria. For example, some of the identified proteins could be components of vaccines against Meningococcus B; against all serotypes; and/or against all pathogenic Neissariae. Identification of sequences and/or against all pathogenic Neissariae. Identification of sequences (Meningococcus B vaccines have failed mainly due to antigen tolerance. Multivalent vaccines have also been tried but none have successfully covercome antigenic variability. The provision of further, complete exposed proteins that may be presumed targets for the immune system and other more variabile readons.
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AAA81490/c
 Sequence 1437668 BP; 344338 A; 353206 C;
                                     other more variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated nucleotide sequences of Neisseria meningitidis which can used in the diagnosis and treatment of N. meningitidis infection a other Neisserial infections, for example, N.gonorrhoea -
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Masignani V, Galeott
Rappuoli R, Pizza M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 7; Page 866-1272; 1760pp; English
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30-APR-1999;
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Galeotti
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99US-0132068
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                                    regions.
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C, Mora
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Ratti G, Scarselli
 385074 G;
 355045
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T; 5 other;
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Best Local Similarity Matches 127; Conserv

Conservative

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Mismatches

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Indels Length

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Gaps

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as a medicament (or

in the manufacture

1437668;

48.8%;

Score 47.2; DB 21; Pred. No. 0.0097;

Query Match

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RESULT
AAA81512
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                                                                                                                  The present invention describes methods of obtaining immunogenic proteins from Nelsseria genomic sequences. AAA81453 to AAA82414 represent specifically claimed Nelsseria meningitidis genomic DNA sequences; AAA81206 to AAA81303 and AAB256620 to AAB25663 represent Nelsseria DNA sequences and their corresponding proteins; AAA81254 AAA81259 and AAA81321 represent PCR primers used in the isolation of Nelsseria meningitidis DNA sequences; and AAA81322 to AAA81323 represent PCR primers used in the isolation of Nelsseria meningitidis brown and AAA81322 to AAA81323 represent PCR primers used in the isolation of Nelsseria meningitidis brown and AAA81322 to AAA81323 represent PCR primers used in the isolation of Nelsseria meningitidis brown and AAA81322 to AAA81323 represent PCR primers used in the isolation of Nelsseria meningitidis brown and AAA81322 to AAA81323 represent PCR primers used in the isolation of Nelsseria meningitidis brown and AAA81322 to AAA81323 represent PCR primers used in the isolation of Nelsseria meningitidis proteins and AAA81323 represent PCR primers used in the isolation of Nelsseria meningitidis proteins and AAA81323 represent PCR primers used in the isolation of Nelsseria meningitidis proteins and AAA81323 represent PCR primers used in the isolation of Nelsseria meningitidis proteins and AAA81323 represent PCR primers used in the isolation of Nelsseria meningitidis proteins and AAA81323 represent PCR primers used in the isolation of Nelsseria meningitidis proteins and AAA81323 represent PCR primers used in the isolation proteins and AAA81323 represent PCR primers used in the isolation proteins and AAA81323 represent PCR primers used in the isolation proteins and AAA81323 represent PCR primers used in the isolation proteins and AAA81323 represent PCR primers used in the isolation proteins and AAA81323 represent PCR primers used in the isolation proteins and AAA81323 represent PCR primers used in the isolation proteins and AAA81323 represent PCR primers used in the isolation proteins and AAA81323
              AAA81452 represent Neisseria meningitidis MenB polynucleotide ORF sequences, which are all used in the exemplification of the present invention. The nucleic acid sequences, protein sequences, and antibodies against them, can be used in the manufacture of a composition. The
                                                                                                                                                                                                                                                                                                                                                    Claim 7; Page 1372-1375; 1760pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                     Isolated nucleotide sequences of Neisseria meningitidis which can be used in the diagnosis and treatment of N. meningitidis infection and other Neisserial infections, for example, N.gonorrhoea -
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Masignani V, Galeo
Rappuoli R, Pizza
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30-APR-1999;
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, Galeotti
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C, Mora
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3545/c
AAF28545 standard; DNA; 62909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             be components of vaccines against Meningococcus B; against all serotypes; and/or against all pathogenic Neissariae. Identification of sequences from the bacterium will also facilitate production of biological probes, particularly organism-specific probes. Attempts to make efficacious Meningococcus B vaccines have failed mainly due to antigen tolerance. Multivalent vaccines have also been tried but none have successfully overcome antigenic variability. The provision of further, complete sequences may provide an opportunity to identify secreted or surface exposed proteins that may be presumed targets for the immune system and which are not antigenically variable or at least more conserved than
Genomic library for identifying diagnostic and therapeutic compositions, and for identifying virulence factors, regula
                                                 WPI; 2001-041427/05
                                                                                                                                                  18-JUN-1999;
                                                                                                                                                                                                                                                                               Moraxella catarrhalis
                                                                                                                                                                                                                                                                                                          Genomic library; bacteria; human upper airway; otitis media; sinusitis; bronchopulmonary; endocarditis; meningitis; ss.
                                                                                                                                                                                                                                                                                                                                                            Genomic fragment
                                                                                                                                                                                                                                                                                                                                                                                             04-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                            AAF28545;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  medicament) for treating, preventing or diagnosing infection due to Neisserial bacteria. For example, some of the identified proteins could
                                                                                                                                                                                16-JUN-2000;
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                                                                                                                 (INCY-) INCYTE GENOMICS INC
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48.5%;
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Pred. No. 0.0013;
1; Mismatches 133;
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Matches 132
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                                                          12-JUN-1998;
12-JUN-1997;
11-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to a Moraxella catarrhalis genomic libra comprising of a combination of I nucleic acid molecules (see AAF28514-AAF2854). The library has a number of uses described in the specification e.g. is useful for aidentifying diagnostic and therapeut compositions. M. catarrhalis (Branhamella catarrhalis) is a large
                                                                                                                                                                                                                                                                                                            Gum gene cluster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 62909 BP; 18449 A; 13798 C; 12744 G; 17918 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    aerobic, gram-negative diplococcus, normally found among the bacterial flora of human upper airways. M. catarrhalis is known to cause acute, localised infections such as otitis media, sinusitis and bronchopulmonary infection and life-threatening, systemic diseases including endocarditis and meningitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             elements and drug targets, comprises Moraxella catarrhalis nucleic
                                                                                                                                                                                                                                                 substrate; lactose; sucrose;
                                                                                                                                                                                                                                                              Xantham gum; gum; exopolysaccharide; gum gene
recombination; Xanthomonas; Sphingomonas; sphi
                                                                                                                                                                                                                                                                                                                                                                         AAV99811;
                                                                                                                                                                                                                                                                                                                                                                                                       AAV99811 standard;
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                                                                                                                                                                                     WO9856942-A1
                                                                                                                                                                                                                  Xanthomonas campestris
                                                                                                                                                                                                                                                                                                                                           14-JUN-1999
           (SHIN-) SHINETSU BIO INC.
(SHIE ) SHINETSU CHEM CO LTD
                                                                                                                        12-JUN-1998;
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les 132; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AATCCAAAAACTGGCGAAGCAATCCAAATTGCAGCCAGCAAAGTACCTAGCTTTAAAGCA
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                                                        98US-0096942.
97US-0049428.
98US-0096867.
                                                                                                                         98WO-US12322
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Pred. No. 0.011;
0; Mismatches 145; Indels 0
                                                                                                                                                                                                                                                   starch; ss.
                                                                                                                                                                                                                                                                 sphingan
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Best Local Similarity
Matches 127; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence of segment of Xanthomonas campestris DNA that contains gene cluster that directs Xanthan biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 16075 BP;
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                                    24-MAR-1987;
                                                                                                                       08-OCT-1987
                                                                                                                                                                                                                                                                                                                                                    Thickening agent; oil recovery; drilling fluid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAN70753;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAN70753 standard;
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                                                                                                                                                                                                 W08705938-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33 atggcattgacgaaagcggagatggccgagcgtctgttcgacgaagtcggcctgaacaag 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cccggtcgcaatcccaagaccggtgaggaaattccgatctcggccaggacggtggtgacc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ggccgtcaggtgaagttgtcgggcttcggcaacttcgatctgcggcgcaagaaccaacgg 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ggcgaaggcctgaagctcaccggcctgttctccgctgagcgccgtcaagcgcccggctcgc
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ilarity 47.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16079
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       139;
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Best Local Similarity 49.6%;
Matches 111; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Virtually all of the segment of Xanthomonas campestris DNA that contains a gene cluster that directs Xanthan biosynthesis (AAN70753), codes for protein products. Each gene is designated by a letter (see Fig 11) and its protein product is designated by that letter preceded by "gp" (AAP70455-67).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Virulence gene; antibacterial; vaccine; bacterial infection; septicemia; bronchopneumonia; rhinitis; wound infection; ss.
                                      Lowery DE,
                                                                                                                                                                                                          09-APR-1999;
10-SEP-1999;
                                                                                                                                                                                                                                                                                                                                   06-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                    19-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAC79661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAC79661 standard;
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24-MAR-1986;
                                                                                                                        (PHAA ) PHARMACIA & UPJOHN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       involved in polysaccharide synthesis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                313
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                                           Fuller TE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Doherty DH,
                                                                                                                                                                                                                                                                                                                                       2000WO-US09218
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86US-0842944.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    273
                                           Kennedy MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Betlach MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
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Pred. No. 0.021;
0; Mismatches 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vanderslice
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                113;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   wide variety of animals. The present invention relates to virulence getrom pasteurellaceae. The present sequence is one such virulence gene. The present sequence is one such virulence gene. The present sequence an inactive gene may in turn be used to produce a vaccine, the inactive virulence gene may in turn be used to produce a vaccine, which is useful for treating bacterial infections such as septicemias,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Attenuated Pasteurellaceae bacteria comprising mutations in virulence genes, useful as a live attenuated vaccine against bacterial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 273 BP; 96 A; 52 C; 66 G; 59 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                      AAA88001 standard;
                                                                                                                                                                                                                                                                        Mycobacterium bovis BCG strain; mycobacterium DNA binding protein MDP1; slow growing acid-fast bacterium protein; immunogenicity; pathogenic acid-fast bacterium; diagnosis; tuberculosis; MAC;
                                                                                                                                                                                                                                                                                                                                                               08-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bronchopneumonias, rhinitis and wound infections.
(SAKA ) OTSUKA PHARM CO LTD (YAMA/) YAMADA T.
                                           29-JAN-1999;
                                                                      28-JAN-2000;
                                                                                                    03-AUG-2000
                                                                                                                              WO200044905-A1
                                                                                                                                                                                                                                Mycobacterium bovis.
                                                                                                                                                                                                                                                          pathogenic acid-fast bacterium; diagnosis; tuberculosis; MAC;
Mycobacterium avium intracellular complex; Hansen's disease; ds
                                                                                                                                                                                                                                                                                                                                  Mycobacterium bovis BCG strain MDP1 encoding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000-647422/62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aacccgcgcactggcgagcagattgacattccggcttcctacg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pages 300-301; 322pp; English.
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265..882
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                                                                                                                                                                                                                                                                                                                                                                                                                       DNA;
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                                                                                                                                                           "Mycobacterium DNA binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 40.6; DI
Pred. No. 0.02;
0; Mismatches
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RESULT 10
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Best Local Similarity
Matches 99; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence encodes the Mycobacterium bovis BCG strain mycobacterium DNA binding protein 1 (MDP1), which has immunogenicity against pathogenic acid fast bacteria. The MDP1 protein can be used diagnosis and treatment of diseases involving pathogenic acid-fast bacteria, such as tuberculosis, Mycobacterium avium intracellular complex (MAC) and Hansen's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Fig 2A; 62pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             such as
                                                                                                                                                                                          Cholesterol oxidase; Streptomyces; enzyme; thermostability; diagnosis; endocrine disease; metabolism; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MATS/) MATSUMOTO
Cholesterol oxidase with high thermostability
                                                                                                     05-JUL-1993;
                                                                                                                                                JP06169765-A
                                                                                                                                                                      Streptomyces sp.
                                                                                                                                                                                                                                                   01-MAR-1995
                                                                                                                                                                                                                                                                                             AAQ70417 standard;
                        P-PSDB;
                                    WPI; 1994-237584/29
                                                                                                                           21-JUN-1994
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                                                         (тоум ) тоуово кк.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium DNA binding protein 1 immunogenic for pathogenic 3-fast bacteria for diagnosis, treatment and prevention of diseases
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                                                                                                                                                                                                                                                                                                                                                               aacccgcgcactggcgag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aacaaagcagagctcattgacgtgctcacacagaaattgggctcggaccgtcggcaggcg 327
                                                                                                                                                                                                                                                                                                                                                                                                           ctgaagctcaccggcctgttctccgctgagcgcctcaagcgcccggcccggccgc
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                                                                                                                                                                                                                            cholesterol oxidase
                                                                                                                                                                                                                                                   (first entry)
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                                                                                                     93JP-0165558.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     232 A; 300 C; 346 G; 148 T; 0 other;
                                                                                                                                                                                                                                                                                               DNA;
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                                                                                                                                                                                                                                                                                               ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 39.6; DB Pred. No. 0.071;
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    useful
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Matches 120
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                                                                                                                                                                                                                                                                                                                                                                                                                     1457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1277
  Claim 8;
                         Cholesterol oxidase with high thermostability - diagnosis of endocrine diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1217
                                                                        WPI; 1994-237584/29
                                                                                                                       05-OCT-1992;
                                                                                                                                               05-JUL-1993;
                                                                                                                                                                        21-JUN-1994.
                                                                                                                                                                                               JP06169765-A.
                                                                                                                                                                                                                     Streptomyces
                                                                                                                                                                                                                                               diagnosis;
                                                                                                                                                                                                                                                         Cholesterol oxidase;
                                                                                                                                                                                                                                                                                 Streptomyces cholesterol oxidase
                                                                                                                                                                                                                                                                                                         01-MAR-1995
                                                                                                                                                                                                                                                                                                                                  AAQ70418;
                                                                                                                                                                                                                                                                                                                                                        AAQ70418 standard;
                                                            P-PSDB; AAR60325
                                                                                               (TOYM ) TOYOBO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ctggcgagcagattgacattccggcttcctacggcgttcgtatctccgctggctccctgc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                acgacgccgcgacggaccgcgaagctcaactggacccgtgaccagaacgcccccgcgg
  Page 11-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Page 9-11; 15pp; Japanese.
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                                                                                                                                                                                                                                              endocrine
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                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                        92JP-0266130
                                                                                                                                               93JP-0165558
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15pp;
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                                                                                                                                                                                                                                             Streptomyces; disease; metal
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Pred. No. 0.
                                                                                                                                                                                                                                               metabolism;
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                                                                                                                                                                                                                                                         enzyme;
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stability
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                                   Disclosure; Page 19-21; 23pp; Japanese
                                                                                                              WPI; 1996-479904/48
P-PSDB; AAW08930.
                                                                                                                                                                                                                                                             JP08242860-A.
                                                                                                                                                                                                                                                                                    Streptomyces
                                                                                                                                                                                                                                                                                                            Cholesterol oxidase; mutation; thermal stability; substitution; ss.
                                                                                                                                                                                                                                                                                                                                     Cholesterol oxidase coding sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cholesterol oxidase is used for measurement of cholesterol which is an index for the diagnosis of endocrine diseases and abnormal metabolism. The enzyme is obtained by addiseases and residues to the N-terminus of cholesterol oxidase derived from Streptomyces sp. SA-COO, which shows the same activity as that of the naturally occurring enzyme, but has higher thermostability. Cholesterol
                                                                                                                                                                               07-MAR-1995;
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                                                                                                                                                     (TOYM ) TOYOBO KK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            212 acctcgtttcgaagatcgcccagaagtccaacctgaccaaggctcaggccgaggctgctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tctacgtgaccgac 1473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tgaagaaggccgtc 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gcggctgcgtcctgggcaaggcgacgacgactacggccgcgtcgccggttacaagaacc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acgacetetteggeacceagetgaaggeettegeegaegaettetgetaeeaccegeteg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ccggcctgttctccgctgagcgcgtcaagcgcccggctcgcaccggccgcaacccgcgca 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tcaacgcagccaaggcgctgttcgaccggatcaacaaggcgaacggcacgatctaccggt 1339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              acgacgccgcgacggaccgcgcgaagctcaactggacccgtgaccagaacgccccccgcgg 1279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120;
                                                                         cholesterol oxidase enzyme -
y than the parent enzyme, usef
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                    sp.
                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                               95JP-0047339
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                                                                                                                                                                                                                                                                                       SA-COO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.68;
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Pred. No. 0
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                                                                         ne - having higher thermal useful in cholesterol det
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 217 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   134;
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This sequence encodes wild type cholesterol oxidase. cholesterol oxidases may be prepared by mutation of

Modified

sequence. Mutant cholesterol oxidases pref. have amino acid substitutions at positions 103Ser, 121Val, 135Arg and/or 145Val (see also AAW08931-36). The modified enzymes have higher thermal stability than the parent enzyme.

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RESULT 4
AAH27164
AAH
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  This invention relates to a pregnenolone oxidase, pregnenolone in the presence of an enzyme to form
                                                                         Disclosure;
                                                                                                                                                                                         WPI; 2001-297396/31.
P-PSDB; AAB97267.
                                                                                                                                                                                                                                                                                                            06-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                         06-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                     21-MAR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      JP2001069991-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pregnenolone oxidase; progesterone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAH27164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAH27164 standard; DNA; 1638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1520 tctacgtgaccgac 1533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1280 acgacgccgcgacggaccgcgcgaagctcaactggacccgtgaccagaacgcccccgcgg 1339
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                                                                                                                                                                                                                                                         (TOYM ) TOYOBO KK.
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Local Similarity 47.2%;
les 120; Conservative
                                                                                                                   pregnenolone oxidase used for the reparation of progesterone -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ctggcgagcagattgacattccggcttcctacggcgttcgtatctccgctggctccctgc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ttaacgccttccaggatgtgttcgtcgaggctatgaagtccggcgaaggcctgaagctca 331
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                                                                      Page 12-14;
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                                                                                                                                                                                                                                                                                                            99JP-0251825
the presence
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/product= "Pregnenolone oxidase"
/note= "No stop codon given"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                               25pp; Japanese
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Pred. No. 0.08
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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                                                                                                                                           measurement of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hydrogen peroxide;
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).087;
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which reacts
progesterone
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                                                                                                                                           pregnenolone
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AAB97268 - AAB97274. The enzyme can be used for the measurement of
pregnenolone and the preparation of progesterone. The present sequence
represents DNA encoding wild type pregnenolone oxidase isolated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Differentiation; heart muscle cell; cytokine; tr
proliferation; surface antigen; heart disease; co
bone marrow; umbilical blood cell; heart muscle
myocardial infarction; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1400
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                  Cells capable of differentiating into cardiomyocytes and originating bone marrow or umbilical blood cells for study of cardiomyocyte differentiation and treatment of heart disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1520
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hydrogen peroxide. Also included in the invention are modified
                                                                                                 WPI; 2001-425655/45.
P-PSDB; AAB99920.
                                                                                                                                                                                 Umezawa A,
                                                                                                                                                                                                                                                            28-FEB-2000;
                                                                                                                                                                                                                                                                                28-DEC-1999;
                                                                                                                                                                                                                                                                                                                        02-NOV-2000; 2000WO-JP07741
                                                                                                                                                                                                                                                                                                                                                               05-JUL-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH44356;
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                                                                                                                                                                Yamada
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nes 120; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tgaagaaggccgtc 465
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                                                                                                                                                                                                                                                                2000WO-JP01148
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                                                                                                                                                                                                                        HAKKO KOGYO
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Pred. No. 0.08
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No. 0.087;
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Disclosure; Page 100-102; 187pp; Japanese.

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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 6.5
Best Local Similarity 56.4
Matches 92; Conservative
WPI; 2001-425656/45
                                        Umezawa A,
Yamada Y;
                                                                                                                                     28-DEC-1999; 99JP-0372826.
28-FEB-2000; 2000WO-JP01148.
02-NOV-2000; 2000WO-JP07741.
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                                                                                                                                                                                                                        27-DEC-2000; 2000WO-JP09323.
                                                                                                                                                                                                                                                                                                         WO200148151-A1.
                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                      Heart muscle cell; human; cell differentiation; heart disease; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                              Heart muscle cell differentiation related DNA SEQ ID NO: 12.
                                                                                                   (КУОМ ) КУОМА НАККО КОСУО КК.
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                                                           Hata J,
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56.4%;
                                                           Fukuda K,
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Pred. No. 0.12;
0; Mismatches 70; Indels
                                                         Ogawa S,
                                                         Sakurada K,
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                                                                                                                                                     The present invention provides cells originating in the human bone me or umbilical blood cells which are capable of differentiating into cardiomyocytes. These cells are useful in the treatment of diseases involving heart muscle degeneration, such as myocardial infarction, at the study of cardiomyocyte differentiation. The present sequence is an oligonucleotide described in the exemplification of the invention.
                                                                                                                      Sequence 1326 BP; 215 A; 499 C; 414 G; 198 T; 0 other;
                                                                                                                                                                                                                                                                                 Disclosure; Page 106-108; 183pp; Japanese.
                                                                                                                                                                                                                                                                                                                                 Cells capable of differentiating into cardiomyocytes and originating bone marrow or umbilical blood cells for study of cardiomyocyte
                                                                                                                                                                                                                                                                                                                      differentiation and treatment of heart disease
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                                   Score 39; DB 22; Length 1326;
Pred. No. 0.12;
0; Mismatches 70; Indels
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Search completed: December Job time: 4094 sec 20, 2001, 20:02:58

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Result
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Maximum DB seq length: 2000000000
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Listing first 45 summaries
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/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/BCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*
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4 US-09-095-855-200

1 US-08-042-747A-7

US-08-911-853-14

4 US-09-479-409-19

4 US-09-479-409-29

4 US-09-103-840A-2

4 US-09-103-840A-1

5215881-2
    US-09-194-905-7
US-08-110-300A-8
US-08-816-642-8
PCT-US93-08041-8
US-08-810-300A-9
US-08-810-300A-9
US-08-912-794-1
US-08-997-080-191
US-08-997-080-191
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US-08-426-599B-3
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Sequence 1, Appli
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Sequence 29, Appl
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Sequence 7, Appl
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APPLICANT: Pollock, Thomas J. APPLICANT: Mikolajczak, Marcia APPLICANT: Yamazaki, Motohide APPLICANT: Thorne, Linda APPLICANT: Armentrout, Richard W. APPLICANT: Armentrout, Richard W.
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Sequence 3, Appli	Sequence 1, Appli	Sequence 7, Appli	Sequence 7, Appli	7	7,	13,	13,	13,	13,		14	Sequence 14, Appl	Sequence 14, Appl	Sequence 1, Appli	23,	Sequence 1, Appli	Sequence 1, Appli

ALIGNMENTS

	Db 273 ttccgcccggccagaaactcaagga 298	
	QY 433 atctccgctggctccctgctgaagaa 458	
	Db 213 cccggtcgcaatcccaagaccggtgaggaaattccgatctcggccaggacggtggtgacc 272	
	QY 373 accggccgcaacccgcgcactggcgagcagattgacattccggcttcctacggcgttcgt 432	
	Db 153 ggccgtcaggtgaagttgtcgggcttcggcaacttcgatctgcggcgcaagaaccaacgg 212	
	Qy 313 ggcgaaggcctgaagctcaccggcctgttctccgctgagcgcgtcaagcgcccggctcgc 372	
	Db 93 cgfgaggcgaaggaattcgfcgacgcgfttttcgatgtgctgcgcgatgcactggagcag 152	
	Qy 253 gctcaggccgaggctgctgttaacgccttccaggatgtgttcgtcgaggctatgaagtcc 312	
	Db 33 atggcattgacgaaagcggagatggccgagcgtctgttcgacgaagtcggcctgaacaag 92	
	Qy 193 atggcatacaaccaagtctgacctcgtttcgaagatcgcccagaagtccaacctgaccaag 252	
0;		
	Query Match 7.3%; Score 43.6; DB 3; Length 16075; Best Local Similarity 47.7%; Pred No 0 0017.	
	; PUBLICATION INFORMATION: US-09-096-942-1	
	; ORGANISM: Xanthomonas campestris	
	TYPE: DNA	
	; LENGTH: 16075	
	; SOFTWARE: PatentIn Ver. 2.0	
	; NUMBER OF SEQ ID NOS: 2	
	; EARLIER FILING DATE: 1997-06-12	
	CURRENT FILING DATE: 1998-06-12	
	CURRENT APPLICATION NUMBER: US/09/096, 942	
	; FILE REFERENCE: sed list for appl filed from pro appl	
	; TITLE OF INVENTION: Production of Xanthan Gum by Sphingomonas Bacteria	
	; APPLICANT: Armentrout, Richard W	

COMPUTER READABLE FORM:

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Best Local Similarity 47.7%;
Matches 127; Conservative
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SOFTWARE: PatentIn Ver. 2.0
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LENGTH: 16075
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Thorne, Linda
APPLICANT: Armentrout, Richard W
APPLICANT: Armentrout, Richard W
TITLE OF INVENTION: Production of Xanthan Gum by Sphingomonas Bacteria
TITLE OF INVENTION: Carrying Genes from Xanthomonas Campestris
FILE REFERENCE: seq list for appl filed from pro. appl
CURRENT APPLICATION NUMBER: US/09/096,867
CURRENT FILING DATE: 1998-06-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -09-096-867-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EARLIER APPLICATION NUMBER: 60/049,428 EARLIER FILING DATE: 1997-06-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Pollock, Thomas J
APPLICANT: Mikolajczak, Marcia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Yamazaki, Motohide
                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Compound TITLE OF INVENTION: Treatment TITLE OF INVENTION: TOTAL TOTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Tan, Paul
APPLICANT: Visser, Elizabeth
APPLICANT: Skinner, Margot
APPLICANT: Prestidge, Ross
                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        373 accggccgcaaccgcgcactggcgagcagattgacattccggcttcctacggcgttcgt 432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93 cgtgaggcgaaggaattcgtcgacgcgtttttcgatgtgctgcgcgatgcactggagcag 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33 atggcattgacgaaagcggagatggccgagcgtctgttcgacgaagtcggcctgaacaag 92
                                                                                                                                                                        STREET:
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98121
                                                                                                                     Seattle
                                                                                    WA
                                                                                                                                                                   2601 Elliott Avenue,
                                              USA
                                                                                                                                                                                                                       Law Offices of Ann W. Speckman
                                                                                                                                                                                                                                                                                                                                                     Compounds and Methods for 
Treatment and Diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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US-08-042-747A-7
                                                                                                                                                                                           Sequence 7, Applic Patent No. 5487969
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
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ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
                                                    APPLICANM: Scinicariello, Franco
APPLICANM: Hilliard, Julia K.
TITLE OF INVENTION: Cloning and Amplification of Monkey
TITLE OF INVENTION: Virus Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               307
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FILING DATE: 29-AUG-1996
APPLICATION NUMBER: 08/873,970
FILING DATE: 12-JUN-1997
APPLICATION NUMBER: 08/997,362
FILING DATE: 23-DEC-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENGTH:
                                                                                                                                                                                                                                                                                                          GGCGCTCAGTTCAAGGCTGTTGTCTCTG 454
                                                                                                                                                                                                                                                                                                                                              ggctccctgctgaagaaggccgtcaccg 469
                                                                                                                                                                                                                                                                                                                                                                                       AATCCGCGCACCGGCGAGACCGTGAAGGTCAAGCCCACCTCAGTCCCGGCATTCCGTCCC 426
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                                                                                                                                   Black, Darla
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Cox & Smith Incorporated
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STREET: CITY: S

San Antonio Texas

USA

112 East Pecan Street, Suite 2000

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Best Local Similarity
                                                                                                                                                                                             atent No. 6048710 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2452
                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               2512
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LENGTH: 2943 base pairs
TYPE: nucleic acid
                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                           APPLICANT: Gerritse, Gijsbert
APPLICANT: Quax, Wilhelmus J.
                                                                                                                                                                                                                                                                                                           2632 GCAAGAAGGGCACGAGCGCCCTGCTGAGCGCGAAGGTTACCGACGCGGT 2680
                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                              260 ccgaggctgctgttaacgccttccaggatgtgttcgtcgtcgaggctatgaagtccggcgaag 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       200 acaacaagtctgacctcgtttcgaagatcgcccagaagtccaacctgaccaaggctcagg 259
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                                       STREET: 925 Fage
CITY: Palo Alto
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LOCATION:
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TELEPHONE: 210-226-8395
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                  COUNTRY:
                                                                            ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                              gcaacccgcgcactggcgagcagattgacattccggcttcctacggcgt 428
                                                                                                                                                                                                                                                                                                                                                                                                                                        TGGCGGGCGGCGAGGACGCGCGCGGAGGACTTTGACGAGGCCAAGCTGGCGCAGGCGC
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                                                                                                                                                                                                                                                                                                                                                                                                       gcctgaagctcaccggcctgttctccgctgagcgcgtcaagcgcccggctcgcaccggcc 379
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94304-1013
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                                                             E: Genencor International 925 Page Mill Road
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47.68;
                                                                                                                            EXPRESSION EXPRESSION
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Pred. No. 0.081;
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                                                                                                                            SYSTEM FOR ALTERED LEVELS
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US-08-911-853-14
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 14, Appli
Patent No. 6225106
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1950 base pair
                                                PRIOR APPLICATION DATA:
                                                                                               SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor
                                                                                                                                                                                                                                                                                                                                            APPLICANT: Gerritse, Gijsbert
APPLICANT: Quax, Wilhelmus J
TITLE OF INVENTION: EXPRESSIC
TITLE OF INVENTION: EXPRESSIC
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REFERENCE/DOCKET NUMBER: GC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-846-7620
                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 16-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Glaister, Debra J
TTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       632 TACTGGACGCCGCGAGGCACTGAACAACGCGGTGATGCGCAACGAGAAAAAACAGCGCCG 691
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     329 tcaccggcctgttctccgctgagcgcgtcaagcgcccggctcgcaccggcc 379
                                                                FILING DATE
                                                                                                                             COMPUTER: IBM CON
OPERATING SYSTEM:
                                                                                                                                                                                                                                                  STREET: 925 Page
CITY: Palo Alto
                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                         STATE:
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                                                                                                                                                                                                                   COUNTRY:
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                                APPLICATION NUMBER:
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                                                                                                                                                 IBM Compatible
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                                                                                US/09/479,409
                                08/911,853
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Pred. No. 0.28;
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Best Local Similarity 50.3%;
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                                                 TELEFAX: 650-845-6504
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor International
                                                                                                                                                                                          APPLICATION NUMBER: 08/69 FILING DATE: 16-AUG-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,853
                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED TITLE OF INVENTION: EXPRESSION LEVELS
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                                                                                                                        TELECOMMUNICATION INFORMATION:
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TYPE: nucleic acid
STRANDEDNESS: single
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REGISTRATION NUMBER: 33,888
 STRANDEDNESS:
                                                                                                                                                            NAME: Glaister, Debra REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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                                                                                                         TELEPHONE:
                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                        FILING DATE:
                                    ENGTH:
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                nucleic acid
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                                                                                                         650-846-7620
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single
                                   base pairs
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Patent No. 6225106
GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                Query Match
                                                                                                                             Best
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INFORMATION FOR SEQ ID NO:
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APPLICANT: Quax, Wil
TITLE OF INVENTION:
TITLE OF INVENTION:
                                     2942 CCGAGCTCGATGCCCAGGCGGCGGCGACTACAACGTGATCAACCTGCAGCATGCCTGGG 2883
                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 33,888
REFERENCE/DOCKET NUMBER: GC:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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NAME: Glaister, Debra J
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MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: PRIOR APPLICATION DATA:
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269 ctgttaacgccttccaggatgtgttcgtcgaggctatgaagtccggcgaaggcctgaagc 328
                                                                     209 ctgacctcgtttcgaagatcgcccagaagtccaacctgaccaaggctcaggccgaggctg 268
                                                                                                          Local Similarity 50.3%; nes 86; Conservative
                                                                                                                                                                                                                                LENGTH: 17612 base pairs
TYPE: nucleic acid
STRANGENESS: single
                                                                                                                                                                                                                                                                                                                                             TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/479,409
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                                                                                                                                                                                                                     linear
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                                                                                                                                                                                                                                                                                                                                                650-846-7620
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                                                                                                        Score 35; DB 4
Pred. No. 0.87;
0; Mismatches
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Pred. No.
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. 0.87;
                                                                                                                                              DB 4; Length 17612;
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                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09103840A Patent No. 6294328
                                                                                     SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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                                                                                                                                         FILE REFERENCE: 24366-2007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
-09-103-840a-2
                                                                                                           NUMBER OF SEQ ID NOS: SOFTWARE: PatentIn Ver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1785833 gattcgctggcgctatcgcgggtggccgccgaggcaccggaggacaccatcgtgttctgc 1785892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -09-103-840A-2
                                                                                                                                                                                                           TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS
                                                                                                                                                                                                                                                    APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: FLEISCHMAN, APPLICANT: WHITE, Ower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: FRASER, Claire M. APPLICANT: VENTER, John C.
        ORGANISM: Mycobacterium tuberculosis OTHER INFORMATION: H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Mycobacterium tuberculosis
                                                                  ENGTH: 4411529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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US-07-945-283-1/c
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5215881-2/c
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APPLICANT: CHEUNG, ANDREW K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO:2
                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/07945283 Patent No. 5352596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 69; Conserv
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Best Local (
                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
COMPUTER READABLE FORM:
MEDIOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                               TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2180 GGCCTGGGACCCGCGGCGGCGGCGCCTCTCGGCGCCTTCGCCCACCGCCT 2121
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                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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                                                                                 COUNTRY: UZIP: 61604
                                                                                                                                                                     STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                        ADDRESSEE:
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nilarity 54.8%;
Conservative
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                                                                                                                                                          Curtis P. Ribando
15 No. 5352596th University Street
                                                                                                                                                                                                                                                                                         Andrew K. Ronald D.
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Pred. No. 13;
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Length 2721; '

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TITLE OF INVENTION:

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; LOCATION:
US-07-945-283-1
                                                                                                                                                        US-08-426-599B-3
                                                                                                                             Sequence 3, Application US/08426599B Patent No. 5932438
                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                              Patent No. GENERAL II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 8438 base pairs
                                                                    APPLICANT:
                                                                                                                                                                                                               3463
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NAME/KEY:
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                                                       APPLICANT:
                                                                                                 APPLICANT:
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PPLICANT
                                      APPLICANT:
                                                                                                                                                                                                                                                                                      375 cggccgcaacccgcgcactggcgagcagattgacattccggccttcctacggcgttcgtat 434
                                                                                                                                                                                                                                                                                                                                           315 cgaaggcctgaagctcaccggcctgttctccgctgagcgcgtcaagcgcccggctcgcac 374
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REGISTRATION NUMBER: 27976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 199209
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                                                                                                                                                                                                                                                                       GGCCTGGGACCCGCGCGCGGCGGCCTCTCGGCGCTGCTCGCCGCCTTCGCCCACCGCCT 3464
                                                                                                             INFORMATION:
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        Patino-Martin, Cristina
Kalo-Koenova, Eliza I.
del Moral-Juarez, Catalina
Faus-Santasusana, Ignacio
del Rio-Pericacho, Jose-Luis
                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                            Rubio-Susan,
                                                                                  Oriach-Marsal, Juan
Rubio-Susan, Victor
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622..6495
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replace(7010, "g")
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                                                                                                                                                                                           Patent No. 5512669
                                                                                                                                         REDUCTASE
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Best Local Similarity
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TELEFAX: 202-783-6031
INFORMATION FOR SEQ ID NO:
                                              NUMBER OF SEQUENCES: 7
CURRENT DATA:
APPLICATION NUMBER: US/
FILING DATE: 29-AUG-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 624 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Saxe, Stephen A.
REGISTRATION NUMBER: 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/426,599B
FILING DATE: 21-APR-1995
CLASSIFICATION: 435
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell,
                                                                                                                                                      APPLICANT: PEOPLES, OLIVER P.; SINSKEY, ANTHONY J.
TITLE OF INVENTION: GENE ENCODING BACTERIAL ACETOACETYL-COA
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                      344 ccgctgagcgctcaagcgcccggctcgcaccggccgcaac 384
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              APPLICATION NUMBER: 124,570 FILING DATE: 20-SEP-1993
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SYSTEM: PC-DOS/MS-DOS
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NUMBER: 944,488
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th Street, N.W., Suite 701 East
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Pred. No. 0.2;
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FILING DATE: 03-NOV-1992

APPLICATION NUMBER: 566,535

FILING DATE: 13-AUG-1990

APPLICATION NUMBER: 67,695

FILING DATE: 29-JUN-1987

SEQ ID NO:1:

LENGTH: 1524
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5229279-1
;PATENT NO. 5229279
;APPLICANT: PEOPLES, OLIVER P.;SINSKEY, ANTHONY J.
;TITLE OF INVENTION: METHOD FOR PRODUCING NOVEL POLYESTER
Search completed: December 20, 2001, 20:35:15 Job time: 6221 sec
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CURRENT APPLICATION UNBER: US/07/556,535
APPLICATION UNBER: US/07/556,535
FILING DATE: 13-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 67,695
FILING DATE: 29-AUG-1987
                                                                                                                                                                                                                                                 321 cctgaagctcaccggcctgttctccgctgagcgcgtcaagcgcccggctcgcaccggccg 380
                                                                                                                                                                         261 cgaggctgctgttaacgccttccaggatgtgttcgtcgaggctatgaagtccggcgaagg 320
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Match
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Gapop 10.0 , Gapext 1.0
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ALTGNMENTS	AU083552	AZ934220	BF448729	BF513289	AW027166	BF513628	AI052253	AI218020	BF514120	BF058124	AI218830	AI951671	AI187315	BF058235	AW293155	BE361820	BF597133	AW502914	CNS010BS	BE498578	AW678194	AZ578311	BE761429	BE636631	BF194806	BF485321	CNS0091P	AW679463	AQ991749		109917	BE356624	CNS016BR
	AU083552 AU083552	AZ934220 BJ BA000	BF4 4 87 20 7 03 710 W	BF513289 HT-H-BW1-	AW027166 wt72c02 v	BF513628 UT-H-BW1-	AI052253 0721012 x	AI218020 gh21c04.x	UI-H-BW1	7k38f11	AI218830 gg92h11 v	AI951671 wv38a07 v	AI187315 ge26a09 x	BF058235 7k28q01 x	AW293155 UI-H-BW0-	BE361820 DG1 82 BO	BF597133 su95d06 v	AW502914 UT-HF-BP0	AL098770 Drosonhil	BE498578 WHE0971 C	AW678194 WS1 13 E0	AZ578311 21d10 Sho	BE761429 894099A08	BE636631 rockefell	BF194806 7093610 w	WHEN 31	ALOS3013 Drosophil	AW679463 WS1 24 FO	91749 RECORSO	G355574 EM1 18 A	1099174 TP1 38 G	6624 DG1 126	AL106545 Drosophil

JOURNAL MEDLINE COMMENT RESULT 1 AV386687 LOCUS DEFINITION BASE COUNT REFERENCE AUTHORS TITLE ACCESSION VERSION KEYWORDS FEATURES SOURCE ORGANISM source Contact: Yasukazu Nakamura The First Laboratory for Plant Gene Research Kazusa DNA Research Institute Yana 1532-3, Kisarazu, Chiba 292-0812, Japan Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/. Chlamydomonas reinhardtii Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadaceae; Chlamydomonas. 1 (bases 1 to 428) Asamizu,E., Nakamura,Y., Sato,S., Fukuzawa,H. and Tabata,S. Asamizu,E., Nakamura,Y., Sato,S., Fukuzawa,H. and Tabata,S. A large scale structural analysis of cDNAs in a unicellular green alga, Chlamydomonas reinhardtii. I. Generation of 3433 non-redundant expressed sequence tags DNA Res. 6 (6), 369-373 (1999) 20152988 AV386687 428 bp AV386687 Chlamydomonas cDNA clone CM004f12_r, AV386687 EST AV386687.1 GI:6540903 Chlamydomonas reinhardtii. 73 a XhoI" /clone="CM004f12_r" /clone_lib="Chlamydomonas reinhardtii C9" /clone_lib="Chlamydomonas reinhardtii C9" /dev_stage="photoautotrophic growth" /note="Vector: pBluescriptII SK-; Site_1: /organism="Chlamydomonas /strain="C9" Location/Qualifiers db_xref="taxon:3055" 146 c 140 mRNA sequence. reinhardtii C9 Chlamydomonas reinhardtii φ 69 Site_1: EcoRI; Site_2: 29-SEP-2000

51.6 51.8 49.8 46.2

AZ934085 BF483682 BG309663

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TITLE
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   127
                     204 caagtetgacetegtttegaagategeecagaagteeaaeetgaeeaaggeteaggeega 263
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CAAGGCTAAACTTGTGGAGGCGATCGCTACTGAGGTGGGACTGACCAAGGACGTCGCTGC
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Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii
Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
Chlamydomonadaceae; Chlamydomonas.
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DNA Res. 6 (6), 369-373 (1999)
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AV393637 Chlamydomonas reinhardtii C9 Chlamydomonas reinhardtii
CDNA Clone CLO6bOl_r, mRNA sequence.
AV393637 GI:6547853
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Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
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ilarity 51.5%;
Conservative
                                                                         Conservative
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Location/Qualifiers
                                                                                                                                                                                                                  /db_xref="taxon:3055"
/clone="CL06b01_r"
/clone_11b="Chlamydomonas reinhardtii C9"
/dev_stage="photoautotrophic growth"
/not="Vector: pBluescriptII SK-; Site_1:
                                                                                                                                                                                                                                                                                                                /strain="C9"
                                                                                                                                                                                                                                                                                                                                  /organism="Chlamydomonas
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                                                                     Score 59.6; DB 10;
Pred. No. 1.1e-06;
0; Mismatches 129;
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Pred. No. 1.1e-06;
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                                           gaageteaceggeetgtteteegetgagegegteaagegeeegggetegeaeeggeegeaa 383
                                                                                                                                                                                                                                                                    ggctgctgttaacgccttccaggatgtgttcgtcgaggctatgaagtccggcgaaggcct 323
GACCATCGTGGGCTTCGGCACGTTTGAGGTGCGCGAGCGCGCTGCGCGCCAGGGCCGCAA
                                                                                                                                                                                                   GAAGGCCTTTGACTCCCTGATTGGCGGCATTGAGGACGCCCTCATCAACGGTGACCGCGT 122
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Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Asamizu, E., Miura, K., Kucho, K., Inoue, Y., Fukuzawa, H., Nakamura, Y. and Tabata, S.
Generation of expressed sequence tags from low-CO2 and adapted cells of Chlamydomonas reinhardtii
DNA Res. 7 (5), 305-307 (2000)
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Eukaryota; Viridiplantae; Chlorophyta;
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/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2: EcoRI; Site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Chlamydomonas reinhardtii"
/strain="C9"
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/clone="HC029a09_r"
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Pred. No. 1.1e-06;
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AGTTGGCCTGAAGGATGCCGTGAACG
                                                              CCCCAGCACCGGCGCGGTCCTCCAGATCGCCGCCAGCAAGGCCCCCGTGTTCAAGGCCTC
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Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Asamizu,E., Nakamura,Y., Sato,S., Fukuzawa,H. and Tabata,S. A large scale structural analysis of cDNAs in a unicellular green alga, Chlamydomonas reinhardtii. I. Generation of 3433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The First Laboratory for Plant Gene Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AV387318 509 bp mrNA EST 29-SEP-2000 AV387318 Chlamydomonas reinhardtii C9 Chlamydomonas reinhardtii cDNA clone CM019f02_r, mrNA sequence.

AV387318
                                                                                                                                                                                                                                                                                                                                    Similarity 51.5
37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Yasukazu Nakamura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             non-redundant expressed sequence tags DNA Res. 6 (6), 369-373 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Chlamydomonas reinhardtii c9"
/dev_stage="photoautotrophic growth"
/note="Vector: pBluescriptII SK-; Site_1:
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/clone="CM019f02_r"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="C9"
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                          ctccctgctgaagaaggccgtcaccg 469
AGTTGGCCTGAAGGATGCCGTGAACG
                                                                              CCCCAGCACCGGCGCGCTCCTCCAGATCGCCGCCAGCAAGGCCCCCGTGTTCAAGGCCTC
                                                                                                        cccgcgcactggcgagcagattgacattccggcttcctacggcgttcgtatctccgctgg 443
                                                                                                                                                            GACCATCGTGGGCTTCGGCACGTTTGAGGTGCGCGAGCGCGCTGCGCGCCAGGGCCGCAA
                                                                                                                                                                                        gaageteaceggeetgtteteegetgagegegteaagegeeeggetegeaceggeegeaa 383
                                                                                                                                                                                                                                              GAAGGCCTTTGACTCCCTGATTGGCGGCATTGAGGACGCCCTCATCAACGGTGACCGCGT
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Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Grossman,A., Davies,J., Federspiel,N., Harris,E., Lefebvre,P., McDermott,J.P., Siliow,C., Stern,D. and Surzycki,R. Analyses of the Chlamydomonas reinhardtil Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation Vascular Plants; project phase 2 Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chlamydomonas reinhardtii cDNA, BE337777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Durham, NC 27708-1000, USA
Tel: 919 613 8164
Fax: 919 613 8177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Elizabeth H. Harris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chlamydomonadaceae; Chlamydomonas
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                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    xhoi; This library, constructed by John Davies and Jeffrey McDermott, combines cDNAs from CC-1690 cells grown to mid-log phase in TAP (acetate-containing) medium in the light, TAP medium in the dark, HS (minimal) medium in ambient levels of CO2 and HS medium bubbled with 5% CO2. PolyA mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda ZAP II (Stratagene) in the ECORI (5') and XhoI (3') sites. pBluescript II SK- plasmids were excised from the lambda ZAP clones by superinfection with EXASSIST (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al (1996) Genome Research 6: 791-806."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Box 91000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism-"Chlamydomonas reinhardtii"
/strain-"CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
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Best Local :
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444 ctccctgctgaagaaggccgtcaccg 469
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                                                                                                                                                                                                         324 gaageteaeeggeetgtteteegetgagegegteaagegeeeggetegeaeeggeegeaa 383
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                                                                     CCCCAGCACCGGCGCGCTCCTCCAGATCGCCGCCAGCAAGGCCCCCCGTGTTCAAGGCCTC 376
                                                                                                                                                                                                                                                                                                                                                                                                                                             137;
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BG860650.1
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii
Eukaryota; Viridiglantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1024072A08.y1 C. reinhardtii CC-1690, normaliz Chlamydomonas reinhardtii cDNA, mRNA sequence.
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Durham, NC 27708-1000
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919 613 8177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chauser@duke.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism-"Chlamydomonas reinhardtii"
/strain-"CC-1690 wild type mt+ 21gr"
/db_xref-"taxon:3055"
/clone_lib-"C. reinhardtii CC-1690, normalized, Lambda
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Pred. No. 1.3e-06;
0; Mismatches 129;
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Matches 138; Conserv
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53
   TTTGAAAGACGCAGTTAAATAATTTCATT
                                                             gctgaagaaggccgtcaccgagtgacctt 478
                                                                                                                                                                                                                                                                                                                                         caccggcctgttctccgctgagcgcgtcaagcgcccggctcgcaccggcgcaacccggcg 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tgttaacgccttccaggatgtgttcgtcgaggctatgaagtccggcgaaggcctgaagct 329
                                                                                                                                                 AACCGGTAAAGAAATTACAATCGCGGCTGCAAACGTACCTGCTTTCTCTGCTGGTAAGGC
                                                                                                                                                                                                                  cactggcgagcagattgacattccggcttcctacggcgttcgtatctccgctggctccct
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Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bssrfc@bath.ac.uk
This is one of 2,122 random reads from the MI3 library. For annotation of identified clones (BLASTX, BLASTN and mapping coll K12 genome) please see ffrench-Constant et al. 2000, Nu
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A genomic sample sequence of the entomopathogenic bacterium Photorhabdus luminescens W14: potential implications for vi. Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
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/note="Genomic DNA from strain W14 was size
kb) and then cloned into M13 Janus."
https://dx.doi.org/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006
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                                                                                                                                                                                                                                                                                                                                                                  211 GAAGGCCTTTGACTCCCTGATTGGCGGCATTGAGGACGCCCTCATCAACGGTGACCGCGT
                                                                                                                                                                                                                                                             cccgcgcactggcgagcagattgacattccggcttcctacggc 426
                                                                                                                                                                                                                                                                                                                       CAAGGCTAAACTTGTGGAGGCGATCGCTACTGAGGTGGGACTGACCAAGGACGTCGCTGC
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                                                                                                                                                                                                                              CCCCAGCACCGGCGCGGTCCTCCAGATCGCCGCCAGCAAGGCC
                                                                                                                                                                                                                                                                                               al Similarity
118; Conser
Photorhabdus luminescens,
Photorhabdus luminescens
Bacteria; Proteobacteria;
                                                                                                 AQ989976 627 bp DNA GSS 14-AUG-2000
Rfc00661 Photorhabdus luminescens'strain W14 M13 library
Photorhabdus luminescens genomic clone PLG00661, DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
                                                                        AQ989976.1 GI:9648570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chlamydomonas reinhardtii Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadaceae; Chlamydomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Generation of expressed sequence tags from low-CO2 adapted cells of Chlamydomonas reinhardtii DNA Res. 7 (5), 305-307 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AV637329 376 bp mRNA EST 15-DEC-2000 AV637329 Chlamydomonas reinhardtii 5% CO2 Chlamydomonas reinhardtii cDNA clone HC071g01_r 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nakamura, Y. and Tabata, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chlamydomonas reinhardtii
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Chlamydomonas reinhardtii 5% CO2".
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI; The cDNA library was constructed from cells cultured
in a medium with bubbling air containing 5% carbon
dioxide"
a 128 c 116 g 68 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:3055"
/clone="HC071g01_r"
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gamma subdivision;
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2.3e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123;
Bradyrhizobium japonicum.
Bradyrhizobium japonicum
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Bradyrhizobium group; Bradyrhizobium.
                                                                                                                                                                                                        AZ934085 800 bp DNA
BJ_BA0001D18r B. Japonicum
genomic, DNA sequence.
AZ934085
                                                                                                                                              GSS.
                                                                                                                                                                        AZ934085.1 GI:13776145
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If french-Constant, R. H., Waterfield, N., Burland, V., Perna, N.T.

Daborn, P.J., Bowen, D. and Blattner, F. R.

A genomic sample sequence of the entomopathogenic bacterium

Photorhabdus luminescens W14: potential implications for vir

Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
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This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping annotation of identified clones (BLASTX) and mapping annotation and mapping and mappi
                                                                                                                                                                                                                                                                                                                                                                                                                                                         470
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University of Bath
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131 c 137 g 166 t 4 others
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Biochemistry
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                                                                                                                                                                                                                                                          GSS 24-APR-2001
library Bradyrhizobium japonicum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mapping to
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REFERENCE

(bases 1 to 800)

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AUTHORS
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 aacctgaccaaggctcaggccgaggctgctgttaacgccttccaggatgtgttcgtcgag 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGTCCTATCTCGATGATCAAATCCGAACTTGTTCAGCGTATCGCCGAGCACAACCCG 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121;
Contact: Olin Anderson
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research
West Area, Western Regional Research Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clemson University
100 Jordan Hall, Cl
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                1 (bases 1 to 663)
1 (bases 1 to
                                                                                                                                                                                                                                                                                                                                                    Triticum aestivum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; Pooideae;

Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BF483682 663 bp mRNA EST 06-DEC-2000
WHE2336_F03_L06ZS Wheat pre-anthesis spike cDNA library Triticum
aestivum cDNA clone WHE2336_F03_L06, mRNA sequence.
BF483682
                                                                                                                                     Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bread wheat.
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A marker-dense, sequence-ready map of the Bradyrhizobium japonicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clemson University Genomics Institute Clemson University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Wing RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21376150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tomkins, J.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: rwing@clemson.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             157
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/strain="USDA110"
/db_xref="taxon:375"
/clone_lib="B. japonicum BAC library"
/lab_host="E. col1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pIndigo536; Site_1: HindIII" 231 c 241 g 168 t 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.3%;
54.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 49.8; DB 1
Pred. No. 0.00097
0; Mismatches 9
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,, Rausch, C.J.,
                                                             Service, Pacific
                                                                                                                                                                                                of the wheat
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ACCESSION
VERSION
KEYWORDS
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ORGANISM
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ORIGIN
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                                                                                                 AUTHORS
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  atcgcccagaagtccaacctgaccaaggctcaggccgaggctgctgttaacgccttccag 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gatgtgttcgtcgaggctatgaagtccggcgaaggcctgaagctcaccggcctgttctcc 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gacattccggcttcctacggcgttcgtatctccgctggc 444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAAGCCGGTACCAAGACTGCAGCTGCCGACGCCGGCTACAAGGCCGCCGACAAATCCGCT
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                                         Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Be,Y., Anderson,H., Dale,J., Henry,D., Kernodle,,T., Saski,C., Schwartzbeck,J., Simmons,J., Ch
                                                                                                                                                                                                                                                                                                                                             BG309663 831 bp mRNA EST
HVSMEC0011M08f Hordeum vulgare seedling shoot
HVcDNA0003 (Etiolated and unstressed) Hordeum
                                                                                                                                                                Spermatophyta; Magnoliophyta;
                                                                                                                                                                                                                                                               EST
                                                                                                                                                                                                                                                                                  BG309663
BG309663.1
Development of a genetically and
                                                                                                                                                                                        Eukaryota;
                                                                                                                                                                                                                 Hordeum vulgare
                                                                                                                                                                                                                                      barley.
                                                                                                                                                                                                                                                                                                                            HVSMEc0011M08f, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 5105595773
Fax: 5105595818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: oandersn@pw.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              800 Buchanan Street, Albany, CA 94710, USA
                                                                                                                  Triticeae; Hordeum (bases 1 to 831)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    greenhouse. Whole spike with awas trimmed, white, green and yellow anther were collected and total RNA, and poly(A) RNA were prepared, a cDNA library was made, and the CDNA clones were in vivo excised to give pBluescript phagemids in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: EcoRI; Site_2: XhoI; Plants were grown in t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Wheat pre-anthesis spike cDNA library"
/tlssue_type="Spike before anthesis"
/dev_stage="Adult plant"
/lab_host="E: coli SOLR"
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                                                                                                                                                         Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
yta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
                                                                                                                                                                                                                                                                                     GI:13110510
                                                                                                                                          Hordeum.
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physically anchored
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 11;
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                                              Choi, D.W., Main, D. and
                                                               Begum, D., Frisch,
le, S., Palmer, M.,
                                                                                                                                                                                                                                                                                                                                                    vulgare cDNA clone
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EST resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                         Frisch, D.,
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for barley genomics

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- Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part collaboration with the European Drosophila Genome Project (EDC http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre
                                                                                                                                                                           Plasmid Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 1201)
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BACN15K14 of DrosBAC library from
fly), genomic survey sequence.
                                                                                              Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fi
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Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 819.
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100 Jordan Hall, Clemson,
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Contact: Wing RA
                                                                                                                                         Direct Submission
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see http://www.genome.clemson.edu/projects/barley/ To
order a clone see http://www.genome.clemson.edu/orders"
a 276 c 201 g 174 t 4 others
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/cultivar="Morex"
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The University of Georgia Plant Sciences Building, Rm. Tel: 706 542 1805
                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Sorghum.

1 (bases 1 to 493)
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                                                                 Department of Botany
                                                                                   Unpublished (2000)
Contact: Cordonnier-Pratt
                                                                                                                                                                                                                                         Sorghum bicolor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gcgaaggcctgaagctcaccggcctgttctccgctgagcgcgtcaagcgcccggctcgca 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACTCGGAAGGGTCAGCCGCCGCGGCGCCGAGGAGGAAGACGATGAGGAGTGGGAGTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGGTGTTCGACCCGGAGGCCGCGGTGTTGTCCAGCGGCGAGAGTAGCGGCATGAGCAGCG 177
                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA sequence.
BI099174
BI099174.1 GI:
EST.
                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Pantcoideae; Andropogoneae; Sorghum.
Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for high quality sequence 20. Three-prime sequences, which are obtained with PolyTMix or T
                                                                                      The University of Georgia Plant Sciences Building, Frel: 706 542 1860 Fax: 706 542 1805
                                                                                                                                                                                                                  An EST database from Sorghum: 
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IP1_38_G12.g1_A002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BI099174
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Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequenting
                                                                Email: mmpratt@uga.edu
                                                                                                                                                                                            Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                           Klein, R.R., Cordonnier-Pratt, M.-M., Gingle, A.,
                                                                                                                                                                                                                                                                                                                                                                                     Sorghum bicolor
                                                                                                                                                                          Department of Botany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ĺS
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/note="Organ: 5-day-old dark-grown seedlings; Vector:
/note="Organ: 5-day-old dark-grown seedlings; Vector:
Lambda Zap: Site_1: XhoI; Site_2: EcoRI; The library was
made from poly-A RNA in the cloning vector lambda ZAP II.
Clones to be sequenced were prepared by mass excision."
a 152 c 160 g 103 t
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/db_xref="taxon:4558"
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Pred. No. 0.1;
0; Mismatches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA
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um bicolor cDNA,
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Best Local
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                                                                                                                                       229
                                                                                                                                                                                                                                                                                                                                                                    Match 7.1%;
Local Similarity 47.9%;
TAACCCCCACCGCCCGG
                                                                                         ccggccgcaacccgcgcactggcgagcagattgacattccggcttcctacggcgttcgta
                                                                                                                                                                                                         ACTCGGAAGGGTCAGCCGCCGGCGCCGCCGAGGAGGAAGACGATGAGGAGTGGGAGTTCA
                                                                                                                                                                                                                                        ctcaggccgaggctgctgttaacgccttccaggatgtgttcgtcgaggctatgaagtccg
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                               tctccgctggctccctg
                                                                   TGCGCGGCCTCACCGTCTGATGCATGGCTGCAGCAGCAGCGCCCCTGTTCCCGTGTCCGT
                                                                                                                                                                    gcgaaggcctgaagctcaccggcctgttctccgctgagcgcgtcaagcgcccggctcgca
                                                                                                                                                                                                                                                                                                                                                  123;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          102
                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Immature pannicle 1 (IP1)"
/note="Organ: Developing preanthesis pannicles; Vector:
pBluescript II SK(-) from Lambda Zap II; Site_1: XhoI;
Site_2: EcoRI; The library was made from poly-A RNA in the
cloning vector lambda ZaP II. Clones to be sequenced were
prepared by mass excision."

164 c 172 g 140 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Sorghum bicolor"
/cultivar="BTx623"
365
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                                                                                                                                                                                                                                                                                                                                                                  Score 42.6; DB 11; Pred. No. 0.11;
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Result
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Maximum DB
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Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Issued_Patents_NA:*
1: /cgn2_6/ptodata/
2: /cgn2_6/ptodata/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   441362 seqs, 153338381 residues
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*/cgn2_6/ptodata/1/ina/backfiles1.seq:*
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US-08-188-582-12

US-08-646-715-12

US-08-646-546C-1

US-08-530-524A-1

US-08-530-915A-189

US-09-310-347-3

US-09-310-347-3

US-09-310-347-3

US-09-310-347-3

US-09-317-803-19

US-09-317-803-19

US-09-071-035-325

US-09-071-035-325

US-09-071-035-333

US-09-071-035-333

US-09-071-035-333

US-08-747-221B-30

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US-08-747-221B-30
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US-08-477-396A-3

US-08-426-627-5

US-08-43-731-128

US-08-330-154-1

US-09-134-001C-2393

US-09-231-0178-911

US-09-221-0178-911

US-09-426-290-1

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Sequence 3, Appli
Sequence 1, Appli
Sequence 19, Appl
Sequence 102, App
Sequence 325, App
Sequence 329, App
Sequence 32, Appl
Sequence 30, Appl
Sequence 30, Appl
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Sequence
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25.6	25.6	25.6	25.6	25.8	25.8	25.8	25.8	25.8	25.8	26	26	26.2	26.2	26.2	26.2	26.2	26.2
13.3	13.3	13.3	13.3	13.4	13.4	13.4	13.4	13.4	13.4	13.5	13.5	13.6	13.6	13.6	13.6	13.6	13.6
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US-08-611-928-50	US-08-158-232-50	US-09-371-913A-5	US-09-193-191-3	US-08-961-527-87	US-09-221-017B-731	PCT-US93-10443-7	US-08-471-613-7	US-08-470-925-7	US-08-222-719-7	US-09-134-001C-1781	US-09-222-575-95	US-09-004-838-93	US-09-005-051-26	US-09-005-051-24	US-08-747-221B-26	US-08-747-221B-24	US-09-005-051-32
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ALIGNMENTS

TELECOMUNICATION INFORMATION: TELEPHONE: 202-408-4000 TELEPAX: 202-408-4400 INFORMATION FOR SEQ ID NO: 3: GENERAL INFORMATION: SEQUENCE CHARACTERISTICS: LENGTH: 3092 base pairs TYPE: nucleic acid APPLICANT: Tezuka, Kenich TITLE OF INVENTION: Abili-TITLE OF INVENTION: Abili-NUMBER OF SEQUENCES: 24 CORRESPONDENCE ADDRESS: STREET: 1300 I St. CITY: Washington STATE: D.C. COUNTRY: USA ZIP: 20005-3315 NAME: Hammond, Alan W. REGISTRATION NUMBER: 35,178 REFERENCE/DOCKET NUMBER: 02 ADDRESSEE: Finner ADDRESSEE: Dunner ADDRESSEE: Dunner ADDRESSEE: N.W. STRANDEDNESS: TOPOLOGY: 11r Application US/08426627 Otawara-Hamamoto, Kikuno, Reiko Takeshita, Sunao Amann, Egon Finnegan, Henderson, Farabow, Garrett & cDNA to mRNA double No. 5756664el Protein with Bone Formation Ability and Process for Its Production. 02481-1285-00000 Yoko

ORGANISM: H

Homo sapiens

Placenta

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FEATURE:

NAME/KEY:

LOCATION:

US-08-426-627-3
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                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US-08/146,488
FILING DATE: 29-0CT-1993
APPLICATION NUMBER: US-08/448,388
FILING DATE: 28-MAY-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         quence 3, Application US/08477396A tent No. 5872235
                                                                      TELEFAX: (617) 451-0313 NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
                                                       SEQUENCE CHARACTERISTICS:
                                                                                                         REFERENCE/DOCKET NUMBER: DE 
TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 542-2290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORRESPONDENCE ADDRESS:
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                                                                                                                                                                                TTORNEY/AGENT INFORMATION:
NAME: Heine, Holliday C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89 AACCCTTATAAAACGCGGGTTTTCGCAGAAACATGCGCTAGTATCATTGATGACAACATG 148
                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
TYPE: nuclei
                                                                                                                                                             NAME: Heine, Holliday REGISTRATION NUMBER: 3
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                  nucleic acid
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                                     3126 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ten Post Office
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Liu, Yuan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mat_peptide
join(101..2375)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Weingarten, Schurgin, Gagnebin & Hayes
n Post Office Square
   single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15.2%;
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                                                                                                                                                                                                                                      PCT/US94/12502
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                                                                                                                                               DFCI-333BX
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Pred. No. 1
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US-08-477-396A-3
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Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                  TELEFAX: 202-408-4400 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANTI-SENSE:
FEATURE:
                                                                                                                                                                                                                                                             FILING DATE: 27-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Hammond, Alan W.
REGISTRATION NUMBER: 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
                                                              MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 3253 base pair
                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
FILING DATE: 25-MAR-1
                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               649 AACCATTATCCTAATGGGGTTGTCACTGTTAATTGTGCTCGAATCATCCATGGGAACCAG 708
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               y Match 15.2%;
Local Similarity 59.8%;
hes 49; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                            LENGTH: 3253 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
NAME/KEY:
                                 CELL TYPE: osteosarcoma
                                               ORGANISM:
                                                                                                                                                                                                                 TELEPHONE:
                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                 COPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION:
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                                                Homo sapiens
                                                                                                 linear
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27-MAR-1992
                                                                                  cDNA to mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           No. 5756664el Protein with Bone Formation Ability and Process for Its Production.
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Pred. No. 1.4;
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US-08-943-731-128/c
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US-08-426-627-5
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Patent No. 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 15.2%;
Best Local Similarity 59.8%;
Matches 49; Conservative
                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08,
FILING DATE: 03-OCT-1997
CLASSIFICATION: 435
                                                                                                                  APPLICATION NUMBER: US 07/
FILING DATE: 03 DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: DOYLE LEARY Ph.D., K
REGISTRATION NUMBER: 36,31
REFERENCE/DOCKET NUMBER: 5
                                   TELEX: 831-494
NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 730 base pairs
                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
FILING DATE: 14-MAR-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING
TITLE OF INVENTION: ALTERED TYPE I OR TYPE IX COLLAGEN GENE SEQUENCES
                                                                                    TELEPHONE: 215-965-1284
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FEATURE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
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                                                     TELEPHONE: 215
TELEPHONE: 215-567-2991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COLIGE, ALAIN
EARLY, JAMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEREDA,
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SPOTILA, LORETTA D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PACK, MICHAEL
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join(97..2540)
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                                                                                                                                                                                                                                                                                                                                                               Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            666
                                                                                                                                                                                                          US 07/803,628
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                                     128:
                                                                                                                      9598-27
                                                                                                                                                        KATHRYN
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Pred. No. 1.4;
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US-08-330-154-1
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Query Match 14.5
Best Local Similarity 62.0
Matches 44; Conservative
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                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1257 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                              FEATURE:
                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                  TELEPHONE: 317-276-3169
                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION DATA:
PRIOR APPLICATION UNMBER: US/08/208,925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                            FILING DATE:
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             190 TTT 192
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                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/0 FILING DATE: 09-MAR-1994 APPLICATION NUMBER: US/0
                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 27-OCT-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              314 TCT 312
                                                                                              NAME/KEY:
                                                                                                                                              STRANDEDNESS: double TOPOLOGY: linear
                                                                                                                                                                       LENGTH: 1257 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                             NAME: Hamilton, Amy E
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Indianapolis
STATE: Indiana
                                                                                 LOCATION:
                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
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les 41; Conserv
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Lilly Corporate Center
                                                                                                                                                                                                                                       317-276-1294
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Skatrud, Paul L
                                                                              1..1257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PatentIn Release #1.0, Version #1.25
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E: DNA (genomic)
                                                                                                                             DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Serhat
                   14.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THE FEMA GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEMA GENE OF STAPHYLOCOCCUS EPIDERMIDIS FEMA PROTEIN, AND VECTORS AND MICROORGAN
                                                                                                                                                                                                                                                                                                                                                           US/08/057,163
                                                                                                                                                                                                                                                                                             33,894
                   Score 27.8;
Pred. No. 3
                                                                                                                                                                                                                                                                                  x-8894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 27.8;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ed. No. 2.4;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VECTORS AND MICROORGANISMS COMPRISING
                                DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22;
                              Length 1257;
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0;

Mismatches

27;

0

Gaps

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PATENT NO. 6380370

PATENT NO. 6380370

GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

FILE REFERENCE: GTC-007

CURRENT ELLING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-10-88

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674

SEQ ID NO 2393

LENGTH: 1269

TYPE: DNA
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-2393
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US-09-134-001C-2393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            694 AAACATTATAAAGACCGTGTTTTAGTACCACTAGCCTATATTAACTTTGATGAGTATATA 753
                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           754 GAGGAACTAAA 764
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                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                 APPLICANT: ALA-KOKKO, LEENA, et al.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING
TITLE OF INVENTION: ALTERED TYPE I OR TYPE IX COLLAGEN GENE SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                     PPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               149 GACTAAGCAAA 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     703 AAACATTATAAAGACCGTGTTTTAGTACCACTAGCCTATATTAACTTTGATGAGTATATA 762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89 AACCCTTATAAAACGCGGGTTTTCGCAGAAACATGCGCTAGTATCATTGATGACAACATG 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89 AACCCTTATAAAACGCGGGTTTTCGCAGAAACATGCGCTAGTATCATTGATGACAACATG 148
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                                                                                                                           STREET:
                                                                                  STATE:
                                        COUNTRY: USA
ZIP: 19103-7086
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3, Application US/08943731
). 6265157
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                                                                                                         PHILADELPHIA
                                                                                     PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROCKOP, DARWIN J. SPOTILA, LORETTA D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                           COLIGE, ALAIN
                                                                                                                                                                                                                                                                                                                                                                     PACK, MICHAEL
                                                                                                                                                                                                                                                                                                                                                                                       LARSON,
                                                                                                                                                                                                                                                                                                                         EARLY, JAMES
                                                                                                                                                                                                                                                                                                                                                                                                                                DELTAS, CONSTANTINOS D.
                                                                                                                                                                                                                                                                                                       KORKKO,
                                                                                                                                                                                                                                                                                                                                                                                       ANDREA W.
                                                                                                                                                                                                                                                                                                JARMO
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US-09-221-017B-911/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 911, Application US/09221017B Patent No. 6444799
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                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10606 TTTCAGAAGTGACAGCCTTGACCAAGCTCAGCTGGCTATCCCCTGCCCTCTGAAGGCTGC 10547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 215-567-2991
TELEX: 831-494
INFORMATION FOR SEQ ID NO: 3:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 14-MAR-1994
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                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastESQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Ross, B
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130 TATCATTGATGACAACATGGACTAAGCAAAAGTGCTTGTCCCCTGACCCAAGAAGGATGC 189
            APPLICATION NUMBER: PP11
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP15
                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        190 TTT 192
                                                                              PRIOR APPLICATION DATA:
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: DOYLE LEARY Ph.D., KATHRYN REGISTRATION NUMBER: 36,317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 0 FILING DATE: 03-DEC-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE:
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                                                                                                                                                                                                                                                                                 CITY: Palo Alto
STATE: CA
                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 94304-1018
                                                                                                                                                                                                                                                                                                                  STREET:
                                                                                                               FILING DATE:
                                                                                                                                APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                    755 PAGE MILL ROAD
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                                                                                                                                                                                                                                                                 USA
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                                                                                                                 23-DEC-1998
30-JAN-1998
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                                                                PP1182
                                                                                                                                US/09/221,017B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4;
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                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFOGNATION:
APPLICANT: Berglind Ran Olafsdottir
APPLICANT: Jeffrey Gulcher
TITLE OF INVENTION: HUMAN NARCOLEPSY GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09426290 Patent No. 6410712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/426,290
CURRENT FILING DATE: 1999-10-25
                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE:
                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ
                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NFORMATION FOR SEQ ID NO:
                                                                                                                        NAME/KEY: CDS
                                                                                                                                                           OCATION: (21181)...(21403)
NAME/KEY: CDS
                                                                                                                                                                                              NAME/KEY: CDS
                                                                                      IAME/KEY: CDS
                                                                                                                                                                                                                  EATURE:
                                                                                                                                                                                                                                                                  ENGTH: 168575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 7650 base pair
                                                                                                                                                                                                                                                                                   ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPULE TYPE: UP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/AU98/01023 FILING DATE: 10-DEC-1998 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: 650-813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99 AAACGCGGGTTTTCGCAGAAACATGCGCCTAGTATCATTGATGACAACAT 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39 ATCTTGTCTGATTCGTCTATTTTCAATACCTTCGGGGAAATAGATGTGAAAAACCCCTTATA 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 14.3%;
Local Similarity 53.2%;
es 58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature LOCATION: 1...7650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Monroy, Gladys H
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 27340-20021.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
                                                                                                                                      (95252)...(95430)
(127009)...(127130)
                                                                                                     (101753)...(101996)
                                   (124058)...(124278)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PORYPHYROMONAS GINGIVALIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UNKNOWN
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Pred. No. 8.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51;
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5223394-8
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                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5223394-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 109602 TATTCATATTGGATTGGAGAAAATAAATGTTATAAAGCCTTAAAATTCTCATTTTTATTA 109661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: RECOMBINANT DNA MOLECULE COMPRISING LYMPHOCYTE FUNCTION-ASSOCIATED ANTIGEN 3 PHOSPHATIDYLINOSITOL LINKAGE SIGNAL SEQUENCES: 12
NUMBER OF SEQUENCES: 12
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 57.8
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                                                                                                                                                                                                                                                                                                                                                                  Patent No.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
LOCATION: (128910)...(129139)
                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IHM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 GAAACATGCGCTAGTATCATTGATGACAACATGGACTAAGCAAA 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                134 ATTGATGACAACATGGACTAAGC 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                             837 AGTAATTACAACATGTATTGTGC 859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      777 GGAAGTGTCTGTAAAACGGGTTACAAGACACAGATATGCACTTATACCCATACCATTAGC 836
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                                                                                                    COUNTRY:
                                                                                                                                    CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74 GGAAATAGATGTGAAAACCCTTATAAAACGCGGGTTTTCGCAGAAACATGCGCTAGTATC 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1009
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ARE: PatentIn Release #1.0, APPLICATION DATA:
                                                                                         RY: U.S.A.
20005-3518
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                                                                                                                                                                                                                                             LEGRAND, Michel
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KNIGHT, Mary E.
VAN MONTAGU, Marc
                                                                                                                                                                                                                                                                                                                     FRITIG,
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                                                                                                                                                                                                                                                                                                        Dirk G.
                                                                                                                                                                                                                                                                                                                        Bernard
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Pred. No. 34;
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              Version #1.25
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; MOLECULE TYPE: DNA (genomic) US-08-204-288-3
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Best Local Similarity
Matches 42; Conserv
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TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1244 base pairs
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STRANDEDNESS: single
TOPOLOGY: linear
WOLFORT
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                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                      APPLICANT: Weinzierl, Robert O.J.
TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFS AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 20 TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 861-3000
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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FILING DATE: 09-SEP-1992
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            504 AATCATG 498
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             APPLICATION NUMBER: US/0
FILING DATE: 28-JAN-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                            STREET: 4 Embarcades
CITY: San Francisco
STATE: California
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FILING DATE: 10-SEP-1991
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                                                                                                                                                                                                              USA
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Tanese, Naoko
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Comai, Lucio
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                                                                                                                                                                                                                                                                                                                                                                                                      Wang, Edith
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                                                     US/08/188,582
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Pred. No. 5.6;
0; Mismatches 2
                                                                                           Version
                                                                                             #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (415) 398-324
TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
TELEX: 910 277299
NFORMATION FOR SEQ ID
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                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                               REFERENCE/DOCKET NUMBER: A-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 28-JAN-1994
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                   TELEFAX:
                                                                                                       NAME: Osman, Richard REGISTRATION NUMBER:
                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 09-MA
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STRANDEDNESS: double
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REFERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO
                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 4 Embarcadero Center, Suite 3400 CITY: San Francisco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS, INVENTION: NUCLEIC ACIDS ENCODING TAFS AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                            California
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                                    (415)
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Tanese, Naoko
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Comai, Lucio
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972..3002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dynlact, Brian D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wang, Edith
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                                                                                            INFORMA A RICHARD A 36,627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA
                                                                                                                                                                                                                                09-MAY-1996
 ID NO:
                                    398-3249
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                                                                                      A-57650-2/AJT/RAC
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TYPE: nucleic acid STRANDEDNESS: doub TOPOLOGY: linear

double

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; LOCATION:
US-08-306-546C-1
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US-08-306-546C-1
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                                                                    Matches
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Patent No. 5605797
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Best Local Similarity 66.1%;
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                TELEPHONE: (810)641-1:
TELEFAX: (810)641-027:
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENERAL INFORMATION:
     3567
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                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 65
TELECOMMUNICATION INFORMATION:
TELEPHONE: (810)641-1600
                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/306,5
FILING DATE: September 15, 1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Smith, Deann F.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: BOVING TITLE OF INVENTION: of Use NUMBER OF SEQUENCES: 28
                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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               75 GAAATAGATGTGAAAACCCTTATAAAACGCGGGTTTTCGCAGAAACATGCGCTAGTATCA 134
                                                                  Local Similarity
nes 51; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Michigan
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CITY: Bloomfield Hills
                                                                                                                                                                                                                   TOPOLOGY:
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GATTTGCATGTGATGAGCCTGGCAGCAAAGTGGTATTGCCTTTAACTTGAGATTGAACCA 3626
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                                                                                                                                                                                                                                                nucleic acid
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                                                                                                                                                                                                                                                               3852 base pairs
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                                                                Conservative
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Pred. No.
                                                                Mismatches
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Search completed: December 25, Job time: 144.664 secs
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US-08-530-524A-1
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US-08-530-524A-1
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INFORMATION FOR SEQ
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                                                                                                                            3567 GATTTGCATGTGATGAGCCTGGCAAGCAAGTGGTATTGCCTTTAACTTGAGATTGAACCA 3626
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TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US/08/
FILING DATE: September 19,
CLASSIFICATION: 536
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MEDIUM TYPE: Floppy disk
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APPLICANT: Chen, Hone
APPLICANT: Cavanagh,
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                                                                                           135
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                                                                                                                                                        75 GAAATAGATGTGAAAAACCCTTATAAAACGCGGGTTTTCGCAGAAACATGCGCTAGTATCA 134
                                                                                                                                                                                Local Similarity 56.0%; es 51; Conservation
                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
TOPOLOGY: 11
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OPERATING SYSTEM:
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P.O. Box 828
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Chen, Hong
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SYSTEM: PC-DOS/MS-DOS
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1693.523 Million cell updates/sec
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Copyright (c) 1993 - 2002 Compugen Ltd
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/cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
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| OUS-09-867-701-2315
| OUS-09-874-300-3770
| OUS-09-974-300-3770
| OUS-09-974-105-261
| OUS-09-770-149-122
| OUS-09-774-155-261
| OUS-09-734-674-3
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| OUS-09-734-674-3
| OUS-09-864-761-12306
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        Sequence 3, Appli
Sequence 2306, Ap
Sequence 30755, A
Sequence 3414, Ap
Sequence 14202, A
Sequence 243, App
Sequence 2181, Ap
                                                                                                           Sequence 471, App
Sequence 2315, App
Sequence 2315, App
Sequence 663, App
Sequence 3770, Ap
Sequence 243, App
Sequence 122, App
Sequence 127, App
Sequence 261, App
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ALIGNMENTS

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CURRENT APPLICATION NUMBER: US/09/816,391A
CURRENT FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: JP 00/287688
PRIOR FILING DATE: 2000-09-21
NUMBER OF SEQ ID NOS: 3
SEQ ID NO 1
LENGTH: 600
TYPE: DNA
ORGANISM: Bifldobacterium longum
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US-09-816-391A-1
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APPLICANT: FUJIMORI, Minoru
APPLICANT: TANIGUCHI, Shunichiro
APPLICANT: AWANO, Jun
APPLICANT: YAZAWA, Kazuyuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09816391A Patent No. US20020054865A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: YAZAWA, Kazuyuki
APPLICANT: KANO, Yasunobu
APPLICANT: NAKAMURA, Toshiyuki
APPLICANT: SASAKI, Takayuki
TITLE OF INVENTION: Anaerobic bacterium as a drug
FILE REFERENCE: 2001-WMC/01736
121 ATGCGCTAGTATCATTGATGACAACATGGACTAAGCAAAAGTGCTTGTCCCCTGACCCAA
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mes 192; Conserv
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                                                                                                                 ; OTHER INFORMATION: MAP TO ACOOO062.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = US-09-864-761-16206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-864-761-16206
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                                                                                                                                                                                                                                        SOFTWARE: Annomax
SEQ ID NO 16206
LENGTH: 515
                                     Query Match
Best Local Similarity
Matches 77; Conserv
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PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
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PRIOR APPLICATION NUMBER: GB 24263.6
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                       TYPE: DNA
                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 ATGCGCTAGTATCATTGATGACAACATGGACTAAGCAAAAGTGCTTGTCCCCTGACCCAA 180
13 GGCCATGAAGTGGCTTGACAAGCATAATCTTGTCTGATTCGTCTATTTTCAATACCTTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US01/00666 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 09/608,408 FILING DATE: 2000-06-30 APPLICATION NUMBER: US 09/774,203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US01/00661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US01/00668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US01/00664
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 2000-10-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US01/00662
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 60/234,687 FILING DATE: 2000-09-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US01/00670
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAAGGATGCTTT 192
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                                       Conservative
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49.7%;
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                                                          Score 30.2;
Pred. No. 0.
                                         Mismatches
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                                         Indels
                                                                             Length 515;
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US-09-925-301-471
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                                                                                                                                                                                                                              Sequence 193, Application US/09954456 Patent No. US20020115057A1 GENERAL INFORMATION:
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                                                     CURRENT APPLICATION NUMBER: US/09/954,456
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US/60/233,617
PRIOR FILING DATE: 2000-09-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/9,25,301
CURRENT FILING DATE: 2001-08-10
                                                                                                                                           TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using TITLE OF INVENTION: Sets FILE REFERENCE: 689290-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 1694
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                                     PRIOR APPLICATION NUMBER: US/60/234,052
                                                                                                                                                                                                                APPLICANT: Young,
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LOCATION: (3160)
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NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       149 GACTAAGCAAAAGTGCTTGTCC 170
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APPLICATION NUMBER: US/60/234,923
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Pred. No. 3;
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PRIOR FILING DATE: 2000-09-25

APPLICATION NUMBER: US/60/235,134 FILING DATE: 2000-09-25

2000-09-25

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APPLICANT: Aglate, Paul A.

APPLICANT: Unces, Robert
APPLICANT: Harlocker, Susan L.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.497
CURRENT APPLICATION UNMBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
SOPTWARE: FastSEQ for Windows Version 4.0
LENGTH: 413
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                                                                                                                                              FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(413)

OTHER INFORMATION: n = A,T,C or G

US-09-867-701-2315
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Best Local Similarity
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; ORGANISM: Homo sapiens
US-09-954-456-193
                                                                                    Matches
                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2315, Application US/09867701 Patent No. US20020132237A1
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PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 2276
                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapien
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107 CAGCATGATGCCTCATGCNTGTANTTTCAATACTTTGGGAGGCTTAGGTGGGAGGATCAC 166
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                    35 CATRATCTTGTCTGATTGTCTATTTCAATACCTTCGGGGAAATAGATGTGAAAACCCT 94
                                                                                  Local Similarity es 45; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40 TCTTGTCTGATTCGTCTATTTTCAATACCTTCGGGGAAATAGATGTGAAAACCCCTTATAA 99
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nilarity 50.0%;
Conservative
                                                                                  Conservative
                                                                                                  15.0%;
                                                                              Score 28.8; DE Pred. No. 1.6; 0; Mismatches
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Pred. No. 4.2;
0; Mismatches
                                                                                                                    DB 10;
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US-09-783-590-663
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 663
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 08/420,856
PRIOR FILING DATE: 1995-04-12
PRIOR APPLICATION NUMBER: 08/346,731
PRIOR FILING DATE: 1994-11-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Human Genes, Sequences, FILE REFERENCE: PO-16.2C1
CURRENT APPLICATION NUMBER: US/09/783,590
CURRENT FILING DATE: 2000-02-15
                    OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature LOCATION: (290)
OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature LOCATION: (313)
                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (220)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
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OTHER INFORMATION: n equals a,t,g, or NAME/KBY: misc feature
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                                                                                                                                                                                                                                 LOCATION: (260)
OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                            LOCATION: (248)
OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                               LOCATION: (244)
OTHER INFORMATION: n equals a,t,g, or c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc feature
LOCATION: (173)
OTHER INFORMATION: n equals a,t,g,
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                                                                                                                                       NAME/KEY: misc feature LOCATION: (273)
                                                                                                                                                                       OTHER INFORMATION: n equals a,t,g, or
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OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Homo sapiens
THER INFORMATION: n equals a,t,g, or
                                                                                                                                                                                                                  NAME/KEY: misc feature
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OTHER INFORMATION: n equals a,t,g, or
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LOCATION: (169)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95 TATAAAACGCGGGTT 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  419
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                                                                                                                                                                                                                              Sequence 3770, Application US/09974300 Patent No. US20020146721A1
                                                                                                                                                                                                             GENERAL INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                             APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085.500-US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 60/279,526 PRIOR FILING DATE: 2001-03-27 NUMBER OF SEQ ID NOS: 8481
                                                                                                                                                                          APPLICANT: Berka, Randy M.
APPLICANT: Clausen, Ib Gr
                                               PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
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LOCATION: (413)
OTHER INFORMATION: n equals a,t,g, or
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NAME/KEY: misc feature
LOCATION: (397)
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OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
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OTHER INFORMATION: n equals
NAME/KEY: misc feature
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OTHER INFORMATION: n equals
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NAME/KEY: misc feature
LOCATION: (340)
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OTHER INFORMATION: n equals a,t,g,
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OTHER INFORMATION: n equals a,t,g,
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                                                                                                                                                                                                                                                                                                                                                                       102 CGCGGGTTTTCGCAGAAACATGCGCTAGTATCATTGATGACAACATGGACTAAGCAAAA 160
                                                                                                                                                                                                                                                                                                                                                                                                            175 TTTCCTTTGTCTTTAAATCTCAACACTTTGGGAGACCAAGGTGGGNGGATGGCTTGAAGC 234
                                                                                                                                                                                                                                                                                                                                      235 CAGGAGTTTNTGANCCACCCTGGGGNANCATAAGTGAGNACCCCATGTTTTACAANAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                             42 TTGTCTGATTCGTCTATTTTCAATACCTTCGGGGAAATAGATGTGAAAACCCTTATAAAA 101
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50.4%;
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Pred. No. 1.6;
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                                                                                                                         US-09-770-149-122/c
                                                                       ; GENERAL
                                                                                    Sequence 122, Application Patent No. US20020059663A1
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APPLICANT:
APPLICANT:
APPLICANT:
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INFORMATION:

US/09770149

An, Yong-Qiang Hamilton, Carol Price, Jennifer Gorlach, Jorn

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; TYPE: DNA
; ORGANISM: Bacillus licheniformis
US-09-974-300-3770
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SEQ ID NO 3770
LENGTH: 345
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                                                                                                                                                                    Query Match
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                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/854,883
CURRENT FILING DATE: 2001-05-14
PRIOR APPLICATION NUMBER: US 09/629,644
PRIOR FILING DATE: 2000-07-31
                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 09/487,368
PRIOR FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 389
                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: ANTISENSE MODULATION OF FILE REFERENCE: ISPH-0576
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16482 GAGTTTGGTCTTCTATCCAGGATGCC 16457
                                                                 16542 ATTITCACTCTCCTCCGCAAATCAGAAAACAAAAGCATAATCAAACTGGGGTCTTCTGCA 16483
                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                             ENGTH: 75899
                                117 AAACATGCGCTAGTATCATTGATGAC 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     198 AAGAGAATTTTTTACAAATTTCACAAGTTGTTCAAATTTCAATATTGAAACAGTCGTTTT 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 ATGAAGTGGCTTGACAAGCATAATCTTGTCTGATTCGTCTATTTTCAATACCTTCGGGGA 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77 AATAGATGTGAAAACCCTTATAAAACGCGGGTTTTCGCAGAAACATGCGCTAGTATCATT 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 49.3 les 74; Conservative
                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGCTGTAAAATAGAATAAAAGAACGGTTTT 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Robert McKay
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Brett P. Monia
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                                                                                                                                       Conservative
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Pred. No. 26;
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Pred. No. 2
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                                                                                                                                       Mismatches
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                                                                                                                                                                      Length 75899;
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RESULT 10
US-09-747-155-261/c
Sequence 261, Application US/09747155
Fatent No. US20020151692A1
GENERAL INFORMATION
APPLICANT: Golorgi, Dominique
FIFLE OF INVENTION: No. US20020151692A1el Polypeptides and Nucleic Acids Encoding
FILE REFERENCE: 19904-008 (C009B6834US)
CURRENT APPLICATION NUMBER: US/09/747,155
CURRENT APPLICATION NUMBER: US/09/747,155
       Qy
                                                                                                     ; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(484)
; OTHER INFORMATION: Taxon = 34829; gene = ERU159; pseudogene; Accession DDBJ/EMBL/Gen
US-09-747-155-261
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Best Local Similarity
Watches 42; Conserve
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SEQ ID NO 122
LENGTH: 727
                                        Matches
                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                         SEQ ID NO 261
                                                                                                                                                                                                                                                        SOFTWARE: PatentIn version 3.0
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CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,506
PRIOR FILING DATE: 2000-01-27
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                                                                                                                                                                                                         LENGTH: 48
TYPE: DNA
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APPLICANT:
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APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: thaliana
TILE REFERENCE: 2024 (PARA-013PRV)
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19 GAAGTGGCTTGACAAGCATAATCTTGTCTGATTCGTCTATTTTCAATACCTTCGGGGAAA 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29 GACAAGCATAATCTTGTCTGATTCGTCTATTTTCAATACCTTCGGGGAAATAGATGTGAA 88
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                                                                                                                                                                                                                           484
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Ledford, Brooke L.
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                                      Conservative
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                                                    Score 27.4; DB 10; Pred. No. 5.1;
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; ORGANISM: Arabidopsis thaliana
US-09-938-842A-4498
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APPLICANT: WEL, Ming-Hui et al
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENC
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL001018
                                                                                                              SOFTWARE: FastSEQ
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/09734674 Patent No. US20020081648A1
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Best Local :
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SEQ ID NO 4498
LENGTH: 2000
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                                                                                                                                                  CURRENT FILING DATE:
NUMBER OF SEQ ID NOS:
                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/734,674
CURRENT FILING DATE: 2000-12-13
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PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
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APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
NAME/KEY: misc_feature
LOCATION: (1)...(202001)
                                                           ORGANISM: Human
                                         FEATURE:
                                                                                TYPE: DNA
                                                                                               LENGTH: 202001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91 C 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31 CAAGCATAATCTTGTCTGATTCGTCTATTTTCAATACCTTCGGGGAAATAGATGTGAAAA 90
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40; Conserv
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                                                                                                                               for Windows Version 4.0
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Pred. No. 10;
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                                                                                                                                                                                                                                                                                                                                                               RESULT 14
US-09-864-761-30755/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA; Homo sapien US-09-867-701-2306
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2306
LENGTH: 389
                                                                                                                                                                                                                                                                                                                            Sequence 30755, Application Patent No. US20020048763A1
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Best Local :
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                PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR EILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR EILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR EILING DATE: 2000-08-03
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CURRENT APPLICATION NUMBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
                                                                                                                                  FILE REFERENCE: Acomica-x-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                      APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95 TATAAAACGCGGGTT 109
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Local Similarity 60.0%;
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hes 43; Conserv
APPLICATION NUMBER: GB 24263.6
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Pred. No. 6.4;
0; Mismatches
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Pred. No. 91;
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US-09-938-842A-3414/c ; Sequence 3414, Application ; Patent No. US20020160378A1
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Best Local Similarity
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LENGTH: 1577
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TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TITLE OF INVENTION: SAME, AND METHODS OF USE FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION UNDER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR PELICATION NUMBER: US 60/227,866
PRIOR PILING DATE: 2000-08-24
PRIOR PILING DATE: 2001-01-16
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PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
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APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
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PRIOR APPLICATION NUMBER: PCT/US01/00664
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PRIOR APPLICATION NUMBER: PCT/US01/00666
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OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 6.2

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 6.2

OTHER INFORMATION: NT HIT: M19828.1, EVALUE 0.00e+00

OTHER INFORMATION: EST_HUMAN HIT: R06764.1, EVALUE 0.00e+00

OTHER INFORMATION: SWISSPROT HIT: P04114, EVALUE 0.00e+00
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FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US01/00663
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FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00662
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224
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length: 2000000000
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/BCOMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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US-08-13-5108-100
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US-08-450-497-100
US-09-134-001C-2784
US-08-991-677-3
US-08-91-677-3
US-08-264-578-7
US-08-264-578-7
US-08-264-578-7
US-08-281-193A-41
US-08-486-273A-41
US-08-480-474-41
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US-08-672-850-7
US-08-672-850-10
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US-08-90-227C-1
US-09-198-092-1
US-08-674-887A-5
US-08-951-844-5
US-09-412-347-5
US-09-221-017B-174
US-09-221-017B-174
US-09-221-017B-174
US-09-426-436-1
US-09-426-436-1
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1348.538 Million cell updates/sec
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; MOLECULE TYPE:
US-08-602-359A-31
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US-08-602-359A-31
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                                                                                                    TELEFAX: 619-678-5099 INFORMATION FOR SEQ ID NO:
                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: HAILE, LISA A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 0901
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
TELEPAX: 619-678-5099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                    FILING DATE: February CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
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MEDIUM TYPE: 3.5 INC
COMPUTER: IBM PS/2
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                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 936 NUCLEOTIDES
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TITLE OF INVENTION: ESTERASES
NUMBER OF SEQUENCES: 42
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STREET: 4:
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SOFTWARE: WORD PERFECT 6.0
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STATE: CALIFORNIA
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                                                                                                                                                                                                                                    APPLICATION NUMBER:
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MURPHY, DC
TTD, John
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US-08-672-850-11/c
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                            Sequence 11, Application US/08672850 Patent No. 6140117
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                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 907 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Silva, Robin M.
REGISTION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,850
FILING DATE: 24-JUL-1996
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
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NAME: Silva, Robin M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: NINJURIN NUMBER OF SEQUENCES: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Araki, Toshiyuki
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                                                                                                                         374 GTTGTTGAGCTGGTTGAGT 356
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                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: unknown
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                                                                                                                                                       71 CTTTTTGTTGTGGTGCTGT 89
                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert STREET: Four Embarcadero Center, Suite 3400
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Milbrandt, Jeffrey
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Pred. No. 2.9;
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                                                                                                                                                                                                                                                                                 Length 907;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                Sequence 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Araki, Toshiyuki
                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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TELEFAX: (415) 398-324 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                Turnice 10, Application US/08672850
                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                  APPLICANT: Milbrandt, Jeffr
APPLICANT: Araki, Toshiyuki
TITLE OF INVENTION: NINJURII
NUMBER OF SEQUENCES: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 907 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         374 GTTGTTGAGCTGGTTGAGT 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          434 CCCGAAGGCTGTAATGAAAACATTGATGACCACAGTGAAGAAGACCAAGATGGTGGCTGC 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/672,850 FILING DATE: 24-JUL-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PU
OPERATING SYSTEM:
                                                                                                                                                                   CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71 CTTTTTGTTGTGGTGCTGT 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: San Francisco
APPLICATION NUMBER: FILING DATE: 24-JUI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 58.2 les 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE:
                                                                                                                                                                                                   ADDRESSEE: Flehr, Hohbach, Test, STREET: Four Embarcadero Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        United States
                                                                                                                                                 United States
                                                                                                                                                                                                                                                                                                       Milbrandt, Jeffrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
 24-JUL-1996
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                                                                                                                                                                                                                                                                      NINJURIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Release #1.0, Version #1.30
               US/08/672,850
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Pred. No. 2.9;
                                                                                                                                                                                                                   Test, Albritton & Herbert
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Matches Query Match

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Gaps

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Sequence 1, Application US/08804227C
Patent No. 5876991
                                                                                                                      TELEPHONE: 317-276-2459
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 43280 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-804-227C-1/c
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
REFERENCE/DOCKET NUMBER: X-
                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCI(DOS) Text only
CURRENT APPLICATION DATA:
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TOPOLOGY: unk
MOLECULE TYPE:
                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: THOMAS G. PLANT 1501
STREET: LILLY CORPORATE CENTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1001 base pair:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     528 CCCGAAGGCTGTAATGAAAACATTGATGACCACAGTGAAGAAGACCAAGATGGTGGCTGC 469
                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/804,227C FILING DATE: February 21, 1997 CLASSIFICATION: 435
                                                                                           TOPOLOGY:
                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  468 GTTGTTGAGCTGGTTGAGT 450
                             LOCATION:
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                                               NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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les 46; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: A-63610
                                                                                                                                                                                                                                                                                                                                                                                                                                 46285
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                           CDS
816..14234
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Rosteck, Paul R., Jr.
Sutton, Kimberly L.
                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                             linear
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                                                                         DNA (genomic)
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                                                                                                        single
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Pred. No. 3;
0; Mismatches
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                                                                                               RESULT 7
US-08-674-887A-5/c
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Best Local Sim
Matches 39;
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; NAME/KEY: CDS
; LOCATION: (87)..(1019)
US-09-198-092-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Omura, Mitsuo
APPLICANT: Koma, Yoshinori
APPLICANT: Komatsu, Akira
TITLE OF INVENTION: BETA-CAROTENE HYDROXYLASE GER
FILE REFERENCE: 07898/033001
CURRENT APPLICATION NUMBER: U5/09/198,092A
CURRENT FILING DATE: 1998-11-23
EARLIER APPLICATION NUMBER: JP97/331936
EARLIER FILING DATE: 1997-12-02
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                                                              Sequence 5, Application US/08674887A Patent No. 5939300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 20.3
Best Local Similarity 55.6
Matches 50; Conservative
                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09198092A Patent No. 6214575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Citrus unshiu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENERAL INFORMATION:
APPLICANT: Yano, Masamitsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13262 GACCGCGAACACCGGACAGCGGGCTGGTCCGGGTCAGTTCGTGCAGGTTCAGCGCCGCGTC 13203
                  APPLICANT:
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    APPLICANT:
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NAME/KEY:
LOCATION:
                                                                                                                                                                                                                   111 TGGCGGCCAATAGTCCGACCGCCATGGTGGGGTTTTGTTTTGTTTTACGAGGTTTTGGGTTT 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY:
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                                                                                                                                                                                          97 T 97
                                                                                                                                                                                                                                             37 TGACGACAAAGACCCCGACCGAGATGGTCGGGGTCTTTTTGTTGTGGTGCTGTGACGTGT 96
                                                                                                                                                             51 T 51
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  1158
                                                                                                                                                                                                                                                                                                   Similarity
Robertson, Dan E.
Sanyal, Indrajit
Adhikari, Robert
                                                                                                                                                                                                                                                                                    Conservative
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31232..36067
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20010..31199
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36249..41774
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                                                                                                                                                                                                                                                                                                Score 25.8; D
Pred. No. 4.5;
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Gaps

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TITLE OF INVENTION: CANUMBER OF SEQUENCES: 6

CATALASES

ADDRESSEE:

Jolla

E: Fish & Richardson P.C. 4225 Executive Square, Suite 1400

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US-08-674-887A-5
                                                                                                                                                                                                                                                                                                               US-08-951-844-5/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                            Sequence 5, Application US/08951844
Patent No. 6074860
                                                                                                                                                                                                                                                                ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 2262 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Halle, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM
                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                              TUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                 PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                  856 TTTCGTCGT 848
                                                                                                                                                                                                                                                                                                                                                                                                                                              916 CATTGCCATTACCGTGACAATTACCGACGGTGTGGCCGCCAGCTGTGAGGGCTGCGGTTT 857
                                                                                                                                                                                                                                                                                                                                                                                                               73 TTTTGTTGT 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 CGTAGCGATTACTTCGAGCATTACTGACGACAAAGACCCCGAGCGGAGATGGTCGGGGGTCT 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 03-JUI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Diskette
                                                                                                              CITY: ROSELAND
STATE: NEW JERS
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                COUNTRY: UZIP: 07068
                                                                                                                                                              ADDRESSEE:
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                                                                                                                                                                                 DDRESSEE:
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                                                                                                               NEW JERSEY
                                                                                                                                           E: CARELLA, BYRNE, BAIN, GILFILLAN,
E: CECCHI, STEWART & OLSTEIN
6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2262 base pairs
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                                                                                                USA
                                                                                                                                                                                                                                             Robertson et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Coding Sequence 1...2259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-JUL-1996
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                                                                                                                                                                                                                               Catalases
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60.9%;
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Pred. No. 5.9;
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INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 33
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                       MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: July 3, 199 ATTORNEY/AGENT INFORMATION:
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 TELECOMMUNICATION INFORMATION: TELEPHONE: 619/678-5070
                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                        COUNTRY: US
ZIP: 92037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73 TTTTGTTGT 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                              NAME: Haile, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 09015/002001
                                                                                                                                                                                                                                                                                                      CITY: La Jolla
STATE: .CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Fish & Richardson P.C. STREET: 4225 Executive Square, Suite 1400
TELEPHONE:
                                                                                                                                              FILING DATE:
                                                                                                                                                             APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ce 5, Application US/09412347
No. 6410290
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42; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                         INVENTION
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Adhikari, Robert S.
VENTION: CATALASES
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                                                                                                                                                                                                                        IBM Compatible
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                                                                                                                                                                                                                                            Diskette
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Pred. No. 5.9;
0; Mismatches
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; NAME/KEY:
; LOCATION:
US-08-461-244-1
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   Query Match 19.
Best Local Similarity 68.
Matches 35; Conservative
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Patent No. 5776729
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                                                                                                                                                                                                          TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1586 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 0 L. CITY: Roseland
CTATE: New Jersey
TSA
                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                           FEATURE:
                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HGBER32
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  916 CATTGCCATTACCGTGACAATTACCGACGGTGTGGCCGCCAGCTGTGAGGGCTGCGGTTT 857
                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/461,244
FILING DATE: 05-JUN-1995
CLASSIFICATION: 536
                                                                                                                                       TOPOLOGY:
                                                                                                                                              STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI.
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LOCATION:
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                                                                                                                                     linear
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               19.7%;
68.6%;
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               Score 25.4; D
Pred. No. 7.1;
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Pred. No. 5.9;
   Mismatches
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                             DB 1;
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                             Length 1586;
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Gaps
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US-09-221-017B-174
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                                               Matches
                                                                             Query Match
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Patent No.
                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                          ORGANISM: FEATURE:
                                                                                                                                                                                         ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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CITY: Palo Alto
STATE: CA
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                                                                                                                                                                                                                       MOLECULE TYPE: DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 10-DEC-1998 ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
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APPLICATION NUMBER: PP11
FILING DATE: 31-DEC-1997
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                        NTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
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ADDRESSEE: MORRISON & FOERSTER
                                                                                                                                                                                                                  YPOTHETICAL:
                                                                                                                      NAME/KEY: misc_feature LOCATION: 1...3302
                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PP1546 FILING DATE: 30-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/OFFILING DATE: 23-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM CONTROL OPERATING SYSTEM:
2 GACCTTCTGCTCGTAGCGATTACTTCGAGCATTACTGACGACAAAGACCCCGGACGAGAT 61
                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                              TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE:
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STREET: 755 PAGE MILL ROAD
                                                                                                                                                                                                                                                                                                   ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACTGACGACAAAGACCCCGACCGAGATGGTCGGGGTCTTTTTGTTGTGGTG
                                               50;
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b. 6444799
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94304-1018
                                                                                                                                                                                                                                                                                                                                                                                                                                             Monroy, Gladys H
                                                                                                                                                                                                                                                                                                 3302 base pairs
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                                            Conservative
                                                                                                                                                                                                      UNKNOWN
                                                                                                                                                                                                                                                    circular
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/ENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
EQUENCES: 1120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FastSEQ for Windows Version
                                                                                                                                                                       PORYPHYROMONAS GINGIVALIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IBM Compatible
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                                                                                                                                                                                                                                    DNA (genomic)
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10-DEC-1998
                                                           19.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                            32,430
                                          Score 25.4; DE Pred. No. 9.6; 0; Mismatches
                                              0;
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                                                                        DB 4;
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921 GAAATCCAGCTCCACTCCATCGCTGACAGCATCGCTGATCTCCAACGATTCGGCCTGGAT 980

981 TTGCTGGGCGATATAGTCATGGTGCTCTGCC 1011

GGTCGGGGTCTTTTTGTTGTGGTGCTGTGAC 92

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·08-247-901C-1
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TELEX: TWX 710-581-4766
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 50341
TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              equence 1, Application US/08247901C atent No. 5750384 SENERAL INFORMATION:
                                                                                                            ORGANELLE:
IMMEDIATE SOURCE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/247, FILING DATE: May 23, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/057,531
FILING DATE: April 29, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: April 29, 1
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                              FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                              DESCRIPTION:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 697-5995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
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             IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                               CELL TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Bogosian, Elizabeth A REGISTRATION NUMBER: 39,911
                                                             NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                             INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE
                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Processor (ASCII)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: New York
STATE: New York
COUNTRY: U.S.A.
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                                                                                                                                                                                                                TISSUE TYPE:
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                                                                                                                                                                                                                                                                                               ORGANISM:
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AUTHORS:
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ER: 96
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Best Local Similarity
Matches 36; Conserv
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                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: 08/247,901
                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 697-5995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inc
                                                                                     FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                             DESCRIPTION:
HYPOTHETICAL:
                                                                                                                                                             TOPOLOGY: ]
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                                                                                                                  INTI-SENSE:
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VOLUME:
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PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                TELEFAX: (212) 286-0854 or 286-0082
TELEX: TWX 710-581-4766
                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: M
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER:
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                             DEVELOPMENTAL STAGE:
                                                                     ORGANISM: L5 mycobacteriophage
                                                                                                                                                                                         STRANDEDNESS:
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HAPLOTYPE:
TISSUE TYPE:
                                                          STRAIN
                                            INDIVIDUAL ISOLATE:
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: New York
RY: U.S.A.
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                                                                                                                                                                             linear
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                                                                                                                                              L5 shuttle phasmid sequence
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L5 SHUTTLE PHASMIDS
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                                                                                                                                                                                                                                                                                                                              96700/475
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Pred. No. 34;
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ELL TYPE:

CELL LINE: ORGANELLE: IMMEDIATE SOURCE:

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US-09-075-904-1
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Best Local Similarity bo.,
36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
NAME: Pasqualini, Patricia A.
REGISTRATION NUMBER: 34.894
REFERENCE/DOCKET NUMBER: 96700
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            quence 1, Applic
tent No. 6225066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .1876 ACCGTGACCATCGGCGACTCGCTGATGTCGAGCTGGGACGTATTCCCCCGGCCGT 1929
                                                                 FILING DATE: February 7, ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                               CLASSIFICATION: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                SOFTWARE: Word Processor (ASCII)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POSITION IN GENOME:
                                                                                                                                                    FILING DATE:
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                                                                                                                      FILING DATE:
                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                  APPLICATION NUMBER:
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                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                             SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL:
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                                                                                                                                                                                                                                                                                                                                                            U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           William R. Jacobs, Jr. Barry R. Bloom
                                                                                                                                                                                                                                                                              IBM PC Compatible SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                           Amster, Rothstein & Ebenstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MYCOBACTERIAL SPECIES-SPECIFIC
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               96700/238
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Pred. No. 34;
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US-08-705-557-1
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                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                             tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: TWX 710-581-4766
INFORMATION FOR SEQ ID NO: 1:
                                            COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inc
                                                                                                                                                                                                                                                                                                                                                                                1773 ACCGTGACCATCGGCGACTCGCTGATGTCGAGCTGGGGACGTATTCCCCCGGCCGT 1826
                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PUBLICATION INFORMATION:
                                                                                                                                                                                                  TITLE OF INVENTION:
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ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE TYPE: not applicable CELL TYPE: not applicable CELL LINE: not applicable ORGANELLE: not applicable IMMEDIATE SOURCE: mycobacteric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAGES:
                                                                                         COUNTRY:
                                                                                                            STATE:
                                                                                                                       CITY: New York
                                                                                                                                         STREET:
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                 OPERATING SYSTEM:
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DEVELOPMENTAL STAGE: not a HAPLOTYPE: not applicable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS:
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                                                                                                                                                                                                                                                                                                          Application US/08705557
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA Sequence, Structure and Gene Expression of Mycobacteriophage 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A Phage System
                                                                                                                                         90 Park Avenue
                                                                                                                                                                                                                               Barry R. Bloom
Graham F. Hatf
                                                                                         U.S.A.
                                                                                                                                                                                                                                                              William R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Molecular Microbiology
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                              IBM PC Compatible
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Word Processor (ASCII)
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                                           inch 1.44 Mb storage diskette
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Pred. No. 35;
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; JOURNAL: Molecul
; VOLUME: 7
; PAGES: 395-405
; DATE: 1993
US-08-705-557-1
Search completed: December 25, 2002, 12:59:44
Job time: 89.3364 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 19.5
Best Local Similarity 66.7
Matches 36; Conservative
                                                         DESCRETE DESCRIPTION OF ANTI-SENSE: no ANTI-SENSE: no applicable.
                                                                                                                                                                                                                                                                                                                                                                                                                                     DEVELOPMENTAL STAGE: not applicable
HAPLOTYPE: not applicable
TISSUE TYPE: not applicable
CELL TYPE: not applicable
CELL LINE: not applicable
ORGANELLE: not applicable
IMMEDIATE SOURCE: mycobacteriophage L5 particles
POSITION IN GENOME: entire genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleotide
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: phage genome sequence
HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                                                            LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS: Matfull and Sarkis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/057,
FILING DATE:
APPLICATION NUMBER: 07/833,431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/705,557
                                                                                                                                                                                                                                                     TITLE: A rung
TITLE: Genetics
"TTTLE: Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: mycobacteriophage L5
STRAIN: not applicable
INDIVIDUAL ISOLATE: L5
DEVELOPMENTAL STAGE: not applic
                                                                                                                                                                                                                                                                              TITLE: DNA Sequence, Structure and Gene
TITLE: Expression of Mycobacteriophage L5:
TITLE: A Phage System for Mycobacterial
                                                                                                                                                                                                                                                                                                                                                                                                            AME/KEY:
                                                                                                                                                                                                                                                    Molecular Microbiology
                                                                                                                                        19.5%;
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Pred. No. 35;
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Maximum Match 10
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1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*

5: /cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*

7: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*

8: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*

9: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*

10: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*

11: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*

12: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*

13: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*

14: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*

15: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*

16: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*

17: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*

18: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
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1693.523 Million cell updates/sec
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Copyright (c) 1993 - 2002 Compugen Ltd.
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10 US-09-903-410-31

9 US-09-938-842A-64

12 US-09-935-770A-15

10 US-09-785-770A-15

10 US-09-785-770A-14

10 US-09-529-063-41

10 US-09-529-063-42

10 US-09-529-063-42

10 US-09-93-965-528

10 US-09-93-965-773

10 US-09-983-965-773

10 US-09-914-298-157

10 US-09-915-242-6127

10 US-09-915-242-6127

10 US-09-915-242-6127

10 US-09-915-242-6127

10 US-09-9164-761-195

10 US-09-815-762A-3

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             Sequence 157, App
Sequence 6127, Ap
Sequence 4, Appli
Sequence 3, Appli
Sequence 1959, Ap
Sequence 1959, Ap
                                                                                                                                                                                                                                                                                                          Sequence 1, Appli
Sequence 31, Appl
Sequence 31, Appl
Sequence 64, Appl
Sequence 64, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 14, Appl
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Sequence 42, Appl
Sequence 5288, Ap
Sequence 773, App
Sequence 143, App
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19.1	19.1	19.1	19.1	19.1	19.1	19.1	19.2	19.2	19.2	19.2	19.2	19.4	19.4	19.4	19.5	19./	19.8	19.8	19.8	20.0	20.0	20.2	20.2	20.3	20.3
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US-09-938-842A-5282	US-09-815-242-8046	US-09-815-242-4426	US-09-974-300-715	US-09-867-701-1593	US-09-880-107-1700	US-09-954-456-2053	US-09-954-456-738	US-09-820-893-30	US-09-974-300-4310	US-09-974-300-4253	US-09-880-107-1376	US-09-938-842A-1762	US-09-974-300-2976	US-09-960-352-198	US-09-815-242-9287	US-09-104-792-1	US-09-887-576-663	US-09-938-842A-1836	US-09-969-347-138	US-09-884-889-5	US-09-815-242-6165	US-09-934-868-17	US-09-934-901-7	US-09-764-869-2419	US-09-764-869-2417
Sequence 5282, Ap	Segmence 8046 as		715	7500			Sequence 738. Ann	Segmence 30 and	Secuence Asion as	Seguence April 19	Sequence 1376 An	Sequence 1762. An	Sequence 2976 An	Sequence 198. Ann	Sequence 9287 An	Sequence 1. April	Sequence 663, App	Sequence 1836, Ap	Sequence 138, App	Sequence 5. Appli	Segmence 6165 An		Sequence 7 Appli	Sequence 2419. An	Sequence 2417 An

ALIGNMENTS

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LENGTH: 600
TYPE: DNA
ORGANISM: Bifidobacterium longum
FEATURE:
NAME/KEY: CDS
LOCATION: (193)..(471)
US-09-816-391A-1
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                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09816391A Patent No. US20020054865A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: YAZAWA, Kazuyuki
APPLICANT: KANO, Yasunobu
APPLICANT: NAKAMURA, Toshiyuki
APPLICANT: SASAKI, Takayuki
TITLE OF INVENTION: Anaerobic bacterium as a drug for cancer gene therapy
FILE REFERENCE: 2001-WMC/01736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: FUJIMORI, Minoru
APPLICANT: TANIGUCHI, Shunichiro
APPLICANT: AMANO, Jun
APPLICANT: YAZAWA, Kazuyuki
APPLICANT: KANO, Yasunobu
121 AGTTCAGCG 129
                                                                                                      1 TGACCTTCTGCTCGTAGCGATTACTTCGAGCATTACTGACGACAAAGACCCCGGACCGAGA 60
                                                                                                                                                                               129;
                                                                                                                                                                              Conservative
                                                                                                                                                                       100.0%; Score 129; DB 10; 100.0%; Pred. No. 4.4e-37; tive 0; Mismatches 0;
                                                                                                                                                                                                    Length 600;
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592 AGTTCAGCG

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MOLECULE TYPE: GENOMIC DNA SEQUENCE DESCRIPTION: SEQ ID NO: 31: US-10-027-805-31
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US-09-903-410-31
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Patent No. US20020164725A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 53; Conserv
                             Sequence 31, Application US/09903410 Patent No. US20020146799A1
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APPLICANT: DIVERSA CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 619-678-5099
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
                                                                                                                                      778 GAAGGAGAAGTTTTCGGGCAGATGCTGAGAAGAG 811
                                                                                                                                                                                                         718 GACCTTGAGAACCTACCTCCTGCGCTGATCATAACCGCCGAATACGACCCGCTGAGAGAT 777
                                                                                                                                                                      62 GGTCGGGGTCTTTTTGTTGTGGTGCTGTGACGTG 95
                                                                                                                                                                                                                                            NAME: HAILE, LISA A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 09
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTMARE: WORD PERFECT 6.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/602,359 FILING DATE: <Unknown> ATTORNEY/AGENT INFORMATION:
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TITLE OF INVENTION: ESTERASES
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                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: LINEAR MOLECULE TYPE: GENOMI
                INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/10/027,805 FILING DATE: 21-Dec-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: LA JOLLA
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                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: NUCLEIC ACID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 936 NUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 619-678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OF SEQUENCES: 42
                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAFFIA,
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                                                                                                                                                                                                                                                                                              22.0%;
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; TYPE: DNA
; ORGANISM: Archaeoglobus fulgidus
US-09-903-410-31
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APPLICANT: Zhu, Tong
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLA
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REPERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
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Best Local Similarity 56.4%;
                                                                                                                        Query Match
Best Local S
                                                                                                                                                                                                                                                     SEQ ID NO 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 64, Application US/09938842A Patent No. US20020160378A1
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PRIOR ETLING DATE: 1999-08-24
PRIOR APPLICATION NUMBER: US 08/602,359
PRIOR FILING DATE: 1996-02-16
NUMBER OF SEQ ID NOS: 42
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                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 5379
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                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/300,111
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                                                                                                                                                                                              LENGTH: 2451
TYPE: DNA
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPLICANT:
                                   791
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                                                          TIGTIGTGGTGCTGTGACGTGTTGTCCAACCGTATTATTCCGGACTAGTT 124
                                   TGGCTCCTCGTGCAAGGATTGCTGTTTACAAAGCTCTCTACCGACTTTTTGGAGGCTTTG 850
                                                                                                         Similarity 53.6
59; Conservative
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                                                                                                                            Score 28.4;
Pred. No. 1.
                                                                                                             Mismatches
                                                                                                                                               DB 9;
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                                                                                                                                             Length 2451;
                                                                                                               Indels
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PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066120
PRIOR FILING DATE: 1997-11-21
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Sequence 591, Application US/10052586
Patent No. US20020127584A1
                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/066772
PRIOR FILING DATE: 1997-11-24
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CURRENT FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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OR FILING DATE: 1997-10-17
OR APPLICATION NUMBER: 60/063120
OR FILING DATE: 1997-10-24
OR APPLICATION NUMBER: 60/063121
OR FILING DATE: 1997-10-24
OR APPLICATION NUMBER: 60/063486
OR FILING DATE: 1997-10-21
OR APPLICATION NUMBER: 60/063540
OR FILING DATE: 1997-10-28
OR APPLICATION NUMBER: 60/063540
OR FILING DATE: 1997-10-28
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                                                                                 APPLICATION NUMBER: 60/068017 FILING DATE: 1997-12-18 APPLICATION NUMBER: 60/077450 FILING DATE: 1998-03-10
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APPLICATION NUMBER: 60/
FILING DATE: 1997-10-28
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APPLICATION NUMBER: 60/069870
FILING DATE: 1997-12-17
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APPLICATION NUMBER: 60/063734
FILING DATE: 1997-10-29
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FILING DATE: 1997-12-11
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FILING DATE: 1997-11-24
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Watanabe, Colin
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          1998-03-11
DMBER: 60/077649
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PRIOR APPLICATION NUMBER: 60/083496
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083499
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083559
PRIOR APPLICATION NUMBER: 60/083559
PRIOR FILING DATE: 1998-04-29
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PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082704
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OR FILING DATE: 1998-05-06
OR APPLICATION NUMBER: 60/084414
OR FILING DATE: 1998-05-06
OR APPLICATION NUMBER: 60/084639
OR FILING DATE: 1998-05-07
OR APPLICATION NUMBER: 60/084640
OR FILING DATE: 1998-05-07
OR APPLICATION NUMBER: 60/084643
OR FILING DATE: 1998-05-07
OR APPLICATION NUMBER: 60/085573
OR APPLICATION NUMBER: 60/085579
OR APPLICATION NUMBER: 60/085579
OR APPLICATION NUMBER: 60/085580
OR FILING DATE: 1998-05-15
OR APPLICATION NUMBER: 60/085582
OR APPLICATION NUMBER: 60/085700
OR FILING DATE: 1998-05-15
OR APPLICATION NUMBER: 60/085700
OR FILING DATE: 1998-05-15
OR APPLICATION NUMBER: 60/086023
OR FILING DATE: 1998-05-18
OR APPLICATION NUMBER: 60/086023
OR FILING DATE: 1998-05-18
                                            APPLICATION NUMBER: 60/087098
FILING DATE: 1998-05-28
                                                                                                 APPLICATION NUMBER: 60/086486 FILING DATE: 1998-05-22
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                     APPLICATION NUMBER: 60/087208
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FILING DATE: 1998-04-28
APPLICATION NUMBER: 60/083495
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FILING DATE: 1998-04-22
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APPLICATION NUMBER: 60/0
FILING DATE: 1998-04-21
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FILING DATE: 1998-04-09
APPLICATION NUMBER: 60/081838
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APPLICATION NUMBER: 60/080327
FILING DATE: 1998-04-01
APPLICATION NUMBER: 60/080333
FILING DATE: 1998-04-01
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FILING DATE: 1998-04-08
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1998-05-28
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Best Local Similarity
Matches 50; Conserv
1275 CTGTTTGCTATCTGGGACTAATGCATC 1249
                 102 AACCGTATTATTCCGGACTAGTTCAGC 128
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                                                             AAAAAGACCATCATCTACATTGTCAGGGTCACTATAATCTGTTGCTGACTGTGTTTCCC 1276
                                                                                       ACAAAGACCCCGACCGAGATGGTCGGGGGTCTTTTTGTTGTGGTGCTGTGACGTGTTGTCC 101
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Pred. No. 1
                                                                                                                                 Mismatches
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Query Match

21.6%;

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27.8;

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Length 8121;

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RESULT 6
US-09-785-770A-15/c
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US-09-785-770A-15
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US-09-785-770A-14/c
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SEQ ID NO 15
LENGTH: 5721
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Best Local Similarity
                                                                                                                                                                                             SEQ ID NO 14
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                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: A NOVEL PROTEIN RELATED TO MELANOMA-INHIBITING PROTEIN TITLE OF INVENTION: AND USES THEREOF FILE REFERENCE: 07334-328001 CURRENT APPLICATION NUMBER: US/09/785,770A CURRENT FILING DATE: 2001-02-16
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PRIOR APPLICATION NUMBER: US 09/145,056
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PRIOR FILING DATE: 1999-09-01
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                                                                                           LENGTH: 8121
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: 5'UTR
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NUMBER OF SEQ ID NOS: 24
                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 09/387,462
PRIOR FILING DATE: 1999-09-01
PRIOR APPLICATION NUMBER: US 09/145,056
PRIOR FILING DATE: 1998-09-01
                                                                                                                                                                                                           SOFTWARE: PatentIn Ver. 4.0
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APPLICANT: Barnes, 1
                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 24
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ORGANISM: Homo
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NAME/KEY:
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                   NAME/KEY:
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CDS
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Pred. No. 2
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US-09-529-063-42/c

: Sequence 42, Application US/09529063

: Patent No. US20020102542A1
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US-09-529-063-41
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SEQ ID NO 41
LENGTH: 1422
                                             SOFTWARE: PatentIn Ver. SEQ ID NO 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                              PRIOR APPLICATION NUMBER: JP 9-274674
PRIOR FILING DATE: 1997-10-07
NUMBER OF SEQ ID NOS: 117
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                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/529,063
CURRENT FILING DATE: 2000-04-07
                                                                                                                           PRIOR APPLICATION NUMBER: PCT/JP98/04514
PRIOR FILING DATE: 1998-10-06
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                                                                                                                                                                                                      TITLE OF INVENTION: POLYPEPTIDE, CDNA ENCODING THE POLYPEPTIDE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/529,063
CURRENT FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: PCT/JP98/04514
PRIOR FILING DATE: 1998-10-06
                                                                                                                                                                                                                                         APPLICANT: SHIBAYAMA, SHIRO
APPLICANT: TADA, HIDEAKI
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NUMBER OF SEQ ID NOS: 117
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                                                                                                                                                                                           FILE REFERENCE: Q58769
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APPLICANT: FUKUSHIMA, DAIKICHI
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ORGANISM: Homo sapiens
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mes 60; Conserv
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US-09-983-965-773/c
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                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 5912
SEQ ID NO 5288
LENGTH: 386
                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
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                                         APPLICANT:
                          APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
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LOCATION:
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                       Mathialagan,
                                                       Tao, Nengbing
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(99)..(167)
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                                        Byatt,
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Sequence 773, Application US/09983965
Patent No. US20020137160A1
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APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: NUSCLE AND FAT DEPOSITION
FILE REFERENCE: 37-21(10297)C
CURRENT APPLICATION NUMBER: US/09/983,965
CURRENT FILING DATE: 2001-10-26
                                                                                                        APPLICANT: Warren, Wesley C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 1999-12-15
PRIOR APPLICATION NUMBER: US 60/113,678
PRIOR FILING DATE: 1998-12-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 09/465,231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Clone ID: 39-LIB34-040-Q1-E1-B4
                                                                                                                                                                                                                                                                                                                             108 ATTATTCCGGACTAGTT 124
                                                                                                                                                                                                                                                                                                                                                                 270 ATCCCTCACCTCCTGGGCGATGTGGTTTTCTTGTGGGGCTGTAACCTGCTGGCCCACTTC 329
                                                                                                                                                                                                                                                                                                                                                                                                            48 ACCCCGACCGAGATGGTCGGGGTCTTTTTGTTGTGGTGCTGTGACGTGTTGTCCAACCGT 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCTGCTGCAATTCATTTCTTTCATGATTTATTCGCTCAATGTCTGCAACTGAGTACTTCT 670
INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND INVENTION: MUSCLE AND FAT DEPOSITION
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0020137160A1
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52.6%;
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59.7%;
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Pred. No. 1
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/113,678
PRIOR FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 5912
SEQ ID NO 773
LENGTH: 406
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Best Local Similarity
Matches 46; Conserv
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CURRENT APPLICATION NUMBER: U2/09/983,965
CURRENT FILING DATE: 2001-10-26
PRIOR APPLICATION NUMBER: US 09/465,231
PRIOR FILING DATE: 1999-12-15
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                                             INFORMATION FOR SEQ ID NO: 143:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         218 ATCAATGCCTACCTGGT 202
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                                                                                                                              ATTORREY/AGENT INFORMATION:
NAME: BILLINGS, LUCY J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0459 US
                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/002,485
FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/799,777
FILING DATE: 06-Mar-2001
CIACTETICATION: CIACTETIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC
STREET: 3174 PORTER DRIVE
SEQUENCE CHARACTERISTICS:
LENGTH: 1864 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: HUMAN SIGNAL PEPTIDE-CONTAINING PROTEINS NUMBER OF SEQUENCES: 154
                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: PALO ALTO
                                                                                                                                                                                                                                                                                   CLASSIFICATION: <Unknown>
                                                                   TELEFAX:
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Pred. No. 1
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; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID
US-09-974-298-157
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US-09-974-298-157
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                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                  Sequence 6127, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Best Local 9
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LENGTH: 2096
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                                                                                       APPLICANT:
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CURRENT FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: 60/238,331
                                                                                                                                         APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 194
SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Chen, Huei-Mei
TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER
FILE REFERENCE: PA-0037 P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE:
                                                     APPLICANT:
                                                                        APPLICANT:
                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                 ITLE OF INVENTION: Identification of Essential Genes ITLE OF INVENTION: Prokaryotes
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REFERENCE: ELITRA.011A
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Similarity 54.5%;
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                                                                  Trawick, John D. Carr, Grant J. Yamamoto, Robert T.
                                                                                                                          Wall, Daniel
                                                 Xu, H. Howard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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Pred. No. 2.
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Pred. No. 2
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                                    in
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CURRENT APPLICATION NUMBER: US/09/815,242 CURRENT FILING DATE: 2001-03-21

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TITLE OF INVENTION: NOVEL PROTEIN ZIMDA2
FILE REFERENCE: 00-67
CURRENT APPLICATION NUMBER: US/09/990.017
CURRENT FILING DATE: 2000-11-21
PRIOR APPLICATION NUMBER: US 60/252,374
PRIOR FILING DATE: 2000-11-21
NUMBER OF SEO ID NOS: 6
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 792
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
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                    PEATURE:
OTHER INFORMATION: degenerate sequence
NAME/KEY: misc_feature
LOCATION: 12, 15, 36, 39, 42, 45, 54, 60, 63, 6
LOCATION: 102, 105, 108, 111, 114, 117, 120, 12
LOCATION: 162, 168, 174, 180, 183, 186, 189, 19
LOCATION: 272, 228, 231, 234, 240, 246, 249, 25
LOCATION: 273, 279, 282, 277, Cor G
NAME/KEY: misc_feature
LOCATION: 373, 384, 393, 396, 399, 402, 405, 46
LOCATION: 373, 374, 368, 474, 483, 486, 498, 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; NAME/KEY: CDS
; LOCATION: (1)...(2628)
US-09-815-242-6127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/291,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-23
PRIOR FILING DATE: 2011-02-16
PRIOR FILING DATE: 2011-02-16
PRIOR FILING DATE: 2011-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Conklin, Darrell C.
APPLICANT: Gao, Zeren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/09990017
Patent No. US20020115168A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 59; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Fas
SEQ ID NO 6127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Escherichia coli
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1055 CGGCGTTTGTTCGTCACCGCCGTGAAGTGGTGACCCGTCGTACTATTTTCGA 1106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENGTH: 2628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               995 TCAACATGGTGGCATTGCACCATGGTCAGCCGAAGATCATGAACCTGAAAGACATCATCG 1054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 GGGTCTTTTTGTTGTGGTGCTGTGACGTGTTGTCCAACCGTATTATTCCGGA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21.1%; 52.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 27.2; DB; Pred. No. 2.9; 0; Mismatches
303,
402,
486,
549,
306,
405,
498,
552,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 10;
                                                                                                              , 66,
123,
198,
252,
309,
408,
504,
321,
423,
510,
585,
                                                                                                                  75,
126,
204,
258,
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5, 144, 147, 1
1, 210, 213, 2
3, 261, 264
327,
426,
513,
591,
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153,
219,
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                                                                                                                   Query Match
Best Local Similarity
Matches 31; Conserve
                                                                                                                                                                                                   ; OTHER INFORMATION: n
US-09-990-017-4
                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: 597, 618, 630, 648, 651, 654, 657, 660, 663, 678, 696, 699,
LOCATION: 705, 705, 708, 711, 714, 717, 720, 723, 729, 738, 750, 756,
LOCATION: 765, 771, 777, 780, 783, 789, 792
OTHER INFORMATION: n = A,T,C or G
| |: |:||:|| ||:|
583 TRIGRITYTTYTTRT 566
                                                           64 TCGGGGTCTTTTTGTTGT 81
                                                                                               Conservative
                                                                                                                                              20.8%; Score 26.8; DB 10; 39.7%; Pred. No. 2.6;
                                                                                                                                 18;
                                                                                                                                 Mismatches
                                                                                                                                                              Length 792;
                                                                                                                             0;
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Search completed: December 25, 2002, 12:34:36 Job time: 39.9439 secs